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OM protein - protein search, using sw model

Run on: June 10, 2002, 17:14:13 ; Search time 29.79 Seconds
(without alignments)
894,854 Million cell updates/sec

Title: US-09-297-171-1
Perfect score: 1304
Sequence: 1 NGBRLYRADSRPPDEIKRSG.....QIFSDYQSEVDIYNIRDEL 240

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802:*
1: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
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9: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.*
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19: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1304	100.0	258	6 AAP50190	Sequence encoded b
2	1298	99.5	258	6 AAP50191	Sequence encoded b
3	1298	99.5	382	22 AAU00506	E. coli heat-labli
4	1293	99.2	240	19 AAW65074	E. coli LT-A prote
5	1288	98.8	240	19 AAW65075	E. coli LT-A mutan
6	1287	98.7	259	21 AAY96646	Plant-Optimized E.
7	1283	98.4	259	21 AAY96647	Synthetic E. coli
8	1282	98.3	259	21 AAY96649	Plant-Optimized E.
9	1280	98.2	259	21 AAY96648	Plant-Optimized E.
10	1280	98.2	380	22 AAU00507	E. coli heat-labli
11	1276	97.9	259	21 AAY96650	Plant-Optimized E.

12	1275	97.8	259	21	AA956551	Plant-Optimized E.
13	1190.5	91.3	237	20	AAW67772	E. coli heat labli
14	1183	90.7	236	14	AAAR38728	E. coli heat labile
15	1183	90.7	254	22	AAU14105	peptide sequence f
16	1179	90.4	236	14	AAAR44016	"Lys-63" E.coli he
17	1179	90.4	236	14	AAAR44024	"Glu-114" E.coli h
18	1179	90.4	236	14	AAAR44025	"Lys-114" E.coli h
19	1178	90.3	236	14	AAAR44018	"Tyr-37" E.coli he
20	1178	90.3	236	14	AAAR38732	"Tyr-53" E.coli he
21	1177	90.3	236	14	AAAR44017	"Lys-97" E.coli he
22	1177	90.3	236	14	AAAR38731	"Glu-53" E.coli he
23	1176	90.2	236	14	AAAR38730	"Asp-53" E.coli he
24	1175	90.1	236	14	AAAR44019	"Glu-107" E.coli h
25	1175	90.1	236	14	AAAR44023	"Lys-106" E.coli h
26	1174	90.0	236	14	AAAR44020	"Ser-104" E.coli h
27	1174	90.0	236	14	AAAR44022	"Ser-104" E.coli h
28	1173	90.0	236	14	AAAR44021	"Asp-104" E.coli h
29	1088	83.4	240	14	AAAR38729	Cholera toxin subu
30	1088	83.4	240	19	AAW80807	Amino acid sequenc
31	1088	83.4	258	21	AA956653	Plant-Optimized V.
32	1088	83.4	258	22	AAG65991	Cholera toxin A su
33	1087	83.4	258	21	AA956655	Plant-Optimized mu
34	1085	83.2	240	20	AAW67773	Cholera toxin subu
35	1085	83.2	258	12	AAAR13117	Cholera toxin Al f
36	1084	83.1	240	14	AAAR44027	Lys-63 cholera tox
37	1084	83.1	240	14	AAAR44033	Glu-114 cholera to
38	1084	83.1	258	21	AA956654	Plant-Optimized mu
39	1083	83.1	240	14	AAAR44031	Ser-110 cholera to
40	1082	83.0	240	14	AAAR44028	Lys-97 cholera tox
41	1082	83.0	240	14	AAAR44032	Ala-112 cholera to
42	1081	82.9	240	14	AAAR44030	Asn-107 cholera to
43	1081	82.9	240	14	AAAR44026	Asp-53 cholera tox
44	1081	82.9	258	21	AA956656	Plant-Optimized mu
45	1080	82.8	240	14	AAAR44029	Ser-106 cholera to

ALIGNMENTS

RESULT 1
AAP50190
ID AAP50190 standard; Protein; 258 AA.
XX
AC AAP50190;
XX
DT 30-OCT-1991 (first entry)
XX
DE Sequence encoded by the pig scours heat labile toxin (LT) LTA gene.
XX
KW Pig scours vaccine; toxin; diarrhoea.
XX
OS E. coli NCIB 11932.
XX
PN EP145486-A.
XX
PD 19-JUN-1985.
XX
PF 12-DEC-1984; 84EP-0308620.
XX
PR 12-DEC-1983; 83GB-0033131.
XX
PA (GLAX) GLAXO GROUP LTD.
XX
PI Hayes MV, Harford S, Ross GW;
XX
DR WPI; 1985-148358/25.
XX
DR N-PSDB; AAN50205.
XX
PT New toxoid as inactivated form of toxin for use in vaccines - is
XX obtd. from organism transformed by gene
XX
PS Disclosure; Fig 1; 61pp; English.
XX

CC AAN50205 is the gene sequence of the natural LTA gene. The LTA gene of
 CC the site directed mutant SDM1 (see AAN50206) is inactive. The
 CC inventors claim a vaccine prepn. active against pig scours which
 CC contains an inactivated LTA component, together with additional K88
 CC antigens opt. with whole cells comprising the antigens or contg. the
 CC inactivated LTA.

SQ Sequence 258 AA;

Query Match 100.0%; Score 1304; DB 6; Length 258;
 Best Local Similarity 100.0%; Pred. No. 2.9e-127; Indels 0; Gaps 0;
 Matches 240; Conservative 0; Mismatches 0;

QY 1 NGDRLRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMINLYDHARGTGTGFVRYDDGYV 60
 Db 19 ngdrlradsrppdeikrsgglmprghneyfdrgtqminlydhargtgtgfvyddgyv 78
 QY 61 STSLRSALHLAGOSILSGYSTYYIVYIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIP 120
 Db 79 stslrsalhlagsilsgystyyiviatapnmfnvndvlgvysphpyeqevsalggip 138
 QY 121 YSQIYGWYRVNFGVIDERLHRNREYRDYRNLNIAPAEDGYRLAGFPDPDHOAWREEPWI 180
 Db 139 ysqiygwyrvnfgviderlhrnreyrdyrynlniapaedgyrlagfpdphqawreepwi 198
 QY 181 HPAQCGNSSRTITGDTCNEETQNLSTIYLYREYQSKVKRQIFSDYQSEVDIYNRIRDEL 240
 Db 199 hpaqcgcnssrtitgdtcneetqnlstilyreyqskvkrqifsdysqvsevdynrirdel 258

RESULT 2

ID AAP50191 standard; Protein; 258 AA.

XX AC AAP50191;

DT 30-OCT-1991 (first entry)

DE Sequence encoded by the pig scours heat labile toxin (LT) LTA gene
 DE of the site directed mutant SDM1.

XX KW Pig scours vaccine; toxin; diarrhoea.

XX OS E.coli NCIB 11932.

XX FH Key Location/Qualifiers

FT Misc-difference 79 /note= "Ser in native SQ"

XX PN EP145486-A.

XX PD 19-JUN-1985.

XX PF 12-DEC-1984; 84EP-0308620.

XX PR 12-DEC-1983; 83GB-0033131.

XX PA (GLAX) GLAXO GROUP LTD.

XX PI Hayes MV, Harford S, Ross GW;

XX DR WPI; 1985-148358/25.

XX DR N-PSDB; AAN50206.

XX PT New toxoid as inactivated form of toxin for use in vaccines - is

XX PT obtd. from organism transformed by gene

XX PS Example; Fig 2; 61pp; English.

XX CC AAN50205 is the gene sequence of the natural LTA gene. The LTA gene of
 CC the site directed mutant SDM1 (see AAN50206) is inactive. The
 CC inventors claim a vaccine prepn. active against pig scours which

CC contains an inactivated LTA component, together with additional K88
 CC antigens opt. with whole cells comprising the antigens or contg. the
 CC inactivated LTA.

SQ Sequence 258 AA;

Query Match 99.5%; Score 1298; DB 6; Length 258;
 Best Local Similarity 99.6%; Pred. No. 1.2e-126;
 Matches 239; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NGDRLRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMINLYDHARGTGTGFVRYDDGYV 60
 Db 19 ngdrlradsrppdeikrsgglmprghneyfdrgtqminlydhargtgtgfvyddgyv 78
 QY 61 STSLRSALHLAGOSILSGYSTYYIVYIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIP 120
 Db 79 stslrsalhlagsilsgystyyiviatapnmfnvndvlgvysphpyeqevsalggip 138
 QY 121 YSQIYGWYRVNFGVIDERLHRNREYRDYRNLNIAPAEDGYRLAGFPDPDHOAWREEPWI 180
 Db 139 ysqiygwyrvnfgviderlhrnreyrdyrynlniapaedgyrlagfpdphqawreepwi 198
 QY 181 HPAQCGNSSRTITGDTCNEETQNLSTIYLYREYQSKVKRQIFSDYQSEVDIYNRIRDEL 240
 Db 199 hpaqcgcnssrtitgdtcneetqnlstilyreyqskvkrqifsdysqvsevdynrirdel 258

RESULT 3

AAU00506
 ID AAU00506 standard; Protein; 382 AA.

XX AC AAU00506;

DT 29-AUG-2001 (first entry)

DE E. coli heat-labile enterotoxin (LT) mutant LTS63Y.

XX KW Heat-labile enterotoxin; LT; LTS63Y; Ltdell10/112; mutant;

XX KW detoxified and immunologically active protein; ADP-ribosylation; Gs;
 XX KW endotoxin; diarrhoea; mutein.

XX OS Escherichia coli strain K88ac.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Misc_feature 7 /note= "Important residue for enzymatic activity"

FT Misc_feature 44 /note= "Important residue for enzymatic activity"

FT Region 58..72 /note= "Forms the NAD-binding site"

FT Misc_feature 61 /note= "Important residue for enzymatic activity"

FT Misc-difference 63 /note= "Substitution of wild type Ser to Tyr"

FT Misc_feature 110 /note= "Important residue for enzymatic activity"

FT Misc_feature 112 /note= "Important residue for enzymatic activity"

FT Misc-difference 259 /note= "Encoded by TG"

XX PN WO200119998-A1.

XX PD 22-MAR-2001.

XX PF 15-SEP-1999; 99WO-KR00555.

XX PR 15-SEP-1999; 99WO-KR00555.

XX PA (MOGA-) MOGAM BIOTECHNOLOGY RES INST.

XX XX

PI Park EJ, Kim JS, Chang J, Yum J, Chung S;
 XX WPI: 2001-281524/29.
 DR N-PSDB; AAS01505.
 XX
 XX New detoxified mutants of *Escherichia coli* heat-labile enterotoxin
 PT useful as vaccine for preventing and treating diarrhoea, and as adjuvant
 PT for antibody production
 PT
 XX
 XX Claim 2; Page 39-41; 48pp; English.
 PS
 XX
 XX The present sequence represents *Escherichia coli* heat-labile
 CC enterotoxin (LT) mutant L7S63Y. L7S63Y and L7del110/112 (AAU00507)
 CC are two novel detoxified and immunologically active proteins (LT
 CC mutants) derived by site-directed mutagenesis of the A1 subunit of wild
 CC type LT. The substitution of Ser to Tyr at position 63 in L7S63Y blocks
 CC NAD-binding. Deletion of Glu residues at positions 110 and 112 in
 CC L7del110/112 eliminate the enzymatic activity of LT. The A1 subunit of
 CC wild type LT catalyses ADP-ribosylation of Gs, a GTP-binding protein that
 CC regulates cAMP levels. The resulting increase in cAMP is the cause of
 CC diarrhoea in humans and animals e.g. pigs. The mucosal immunogenicities
 CC of mutant heat-labile endotoxins L7S63Y and L7del110/112 were tested.
 CC Groups of mice were immunised with L7S63Y or L7del110/112. The control
 CC groups received phosphate buffered saline (PBS) alone. The serum and
 CC faecal antibody titres to LT were determined. The results showed that
 CC mice immunised with L7S63Y or L7del110/112 contained high and
 CC comparable level of anti-LT antibodies in sera and faecal extracts
 CC compared with those immunised with wild-type LT. The LT mutants are
 CC useful as a vaccine for preventing and treating diarrhoea and as an
 CC adjuvant for antibody production.
 XX
 XX Sequence 382 AA;
 SQ
 .
 Query Match 99.5%; Score 1298; DB 22; Length 382;
 Best Local Similarity 99.6%; Pred. No. 2.2e-126;
 Matches 239; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NGDRLYRADSRPPDEIKRSGGLMPRGHNEVFDRTQNNINLYDHARTGTGFRYDGYV 60
 DB 19 ngdrllyradsrppdeikrsgglmpgrghneyfdrtqnninlydhartgtgfrvyddgyv 78
 QY 61 STLSLSRAHLAGOSILSGYSTYIVYIATAPNMFNVDLVGYSPPHYEQEVSALGGIP 120
 DB 79 stlslsrsahlagosilsgystyiviyatapnmfnvndvlgyspshpyspheyqsalsggip 138
 QY 121 YSQIYGWYRVNFGVIDERLHNRREYDRYRNINLAPIAEDGYRLAGFPDPHQAWREEPWI 180
 DB 139 ysqiygwyrvnfgviderlhrnreydryrnyrnlnapiaedgyrlagfpdpdqhawreepwi 198
 QY 181 HHAPQCGNSRRTITGTCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIDEL 240
 DB 199 hhappqcgnsrstitgtcneetqnlstlylreyqskvkrqifsdysqsevdinyrirdel 258
 RESULT 4
 AAW65074
 ID AAW65074 standard; protein; 240 AA.
 XX
 AC AAW65074;
 XX
 XX 11-SEP-1998 (first entry)
 DT
 XX
 XX E. coli LT-A protein fragment.
 XX
 XX Heat labile toxin subunit A; LT-A; mutant; immunogen; detoxification;
 KW carrier; adjuvant; prevention; treatment; disease; diarrhoea; vaccine;
 KW infection; enterotoxic.
 XX
 XX *Escherichia coli*.
 OS
 XX Key Location/Qualifiers
 FH Protein 1..241
 FT

FT
 XX
 PN
 XX
 PD
 XX
 XX
 PF 30-OCT-1997; 97WO-IB01440.
 XX
 PR 31-OCT-1996; 96GB-0022660.
 XX
 XX (CHIR-) CHIRON SPA.
 XX
 XX Giuliani MM, Pizza M, Rappuoli R;
 PI
 XX
 DR WPI: 1998-272223/24.
 XX
 XX Mutated *Escherichia coli* heat labile toxin subunit A - is
 PT immunogenic and detoxified relative to wild-type, useful e.g. in
 PT vaccines against *E. coli* enterotoxigenic strains and as an adjuvant
 XX
 XX Disclosure; Page -: 67pp; English.
 XX
 XX This sequence represents a fragment of an *Escherichia coli* heat labile
 CC toxin subunit A (LT-A). This protein is used in a method resulting in a
 CC mutant LT-A protein which has the wild type Ala residue at position 72
 CC changed to an Arg residue resulting in a toxin which retains its
 CC immunogenicity but is detoxified. Detoxification is defined in the
 CC specification as a reduction in toxicity relative to wild-type toxin,
 CC such that any residual toxicity is sufficiently low to allow use as an
 CC effective immunogenic composition in humans without significant side
 CC effects. The protein can be combined with an acceptable carrier in
 CC immunogenic compositions, optionally comprising an adjuvant and/or a
 CC second immunogenic antigen. Such compositions can be administered to
 CC prevent/treat disease in a subject e.g. traveller's diarrhoea in humans.
 CC The protein or compositions are especially administered as vaccines
 CC useful to prevent or treat infections by enterotoxigenic strain of
 CC *E. coli* in mammals (especially humans).
 XX
 SQ Sequence 240 AA;
 .
 Query Match 99.2%; Score 1293; DB 19; Length 240;
 Best Local Similarity 99.2%; Pred. No. 3.7e-126;
 Matches 238; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NGDRLYRADSRPPDEIKRSGGLMPRGHNEVFDRTQNNINLYDHARTGTGFRYDGYV 60
 DB 1 ngdrllyradsrppdeikrsgglmpgrghneyfdrtqnninlydhartgtgfrvyddgyv 60
 QY 61 STLSLSRAHLAGOSILSGYSTYIVYIATAPNMFNVDLVGYSPPHYEQEVSALGGIP 120
 DB 61 stlslsrsahlagosilsgystyiviyatapnmfnvndvlgyspshpyspheyqsalsggip 120
 QY 121 YSQIYGWYRVNFGVIDERLHNRREYDRYRNINLAPIAEDGYRLAGFPDPHQAWREEPWI 180
 DB 121 ysqiygwyrvnfgviderlhrnreydryrnyrnlnapiaedgyrlagfpdpdqhawreepwi 180
 QY 181 HHAPQCGNSRRTITGTCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIDEL 240
 DB 181 hhappqcgnsrstitgtcneetqnlstlylreyqskvkrqifsdysqsevdinyrirdel 240
 RESULT 5
 AAW65075
 ID AAW65075 standard; protein; 240 AA.
 XX
 AC AAW65075;
 XX
 XX 11-SEP-1998 (first entry)
 DT
 XX
 XX E. coli LT-A mutant A72R protein fragment.
 XX
 XX Heat labile toxin subunit A; LT-A; mutant; immunogen; detoxification;
 KW

KW carrier; adjuvant; prevention; treatment; disease; diarrhoea; vaccine;
KW infection; enterotoxic.

XX Escherichia coli.

XX Key Location/Qualifiers

FT Misc-difference 72

FT /label= A72R

FT /note= "Wild type Ala residue is replaced by Arg"

XX WO9818928-A1.

XX 07-MAY-1998.

XX 30-OCT-1997; 97WO-IB01440.

XX 31-OCT-1996; 96GB-0022660.

XX (CHIR-) CHIRON SPA.

XX Giuliani MM, Pizza M, Rappuoli R;

XX WPI; 1998-272223/24.

XX Mutated Escherichia coli heat labile toxin subunit A - is
PT immunogenic and detoxified relative to wild-type, useful e.g. in
PT vaccines against E. coli enterotoxigenic strains and as an adjuvant

XX Claim 3; Page -: 67pp; English.

XX This sequence represents a fragment of a mutant Escherichia coli heat
CC labile toxin subunit A (LT-A) where the wild type Ala residue at
CC position 72 is replaced by an Arg residue resulting in a toxin which
CC retains its immunogenicity but is detoxified. Detoxification is defined
CC in the specification as a reduction in toxicity relative to wild-type
CC toxin, such that any residual toxicity is sufficiently low to allow use
CC as an effective immunogenic composition in humans without significant
CC side effects. The protein can be combined with an acceptable carrier in
CC immunogenic compositions, optionally comprising an adjuvant and/or a
CC second immunogenic antigen. Such compositions can be administered to
CC prevent/treat disease in a subject e.g. traveller's diarrhoea in humans.
CC The protein or compositions are especially administered as vaccines
CC useful to prevent or treat infections by enterotoxigenic strain of
CC E. coli in mammals (especially humans).

CC NOTE: This sequence does not appear in the specification but has
CC been constructed from the wild-type sequence represented in AAW65074.

XX Sequence 240 AA;

Query Match 98.8%; Score 1288; DB 19; Length 240;
Best Local Similarity 98.8%; Pred. No. 1.2e-125;
Matches 237; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 NGDRLYRADSRPDEIKRSGLMPRGHNEYFDRTGTMNINLYDHARGTGTGFVRYDDGYV 60

Db 1 ngdrlyradsrppdeikrsgglmpgrhneyfdrgtgmninlydhargtgtgfvyddgyv 60

QY 61 STSLSLRSAHLAQSGILSGYSTYIIYVIATAPNMENVDVLGVYSPHPYEQEVSALGGIP 120

Db 61 stslsrsahlrgqslsgystyiyviatapnmfndvlgvysphpyeqkvsa199lp 120

QY 121 YSQIYGWYRVNFGVIDERLHRNREYDRYRNLIAPAEDGYRLAGFPDQAWREEPWI 180

Db 121 ysqlygwyrvnfgviderlhnreaydrdyrnlniapaedgyrlagfpdhaqawreepwi 180

QY 181 HHAPOCGNSRRTIGDTCNEETQNLSTIYLYREYQSKVRQIFSDYQSEVDIYNRIDEL 240

Db 181 hhapqcgnsrtritgdctcneetqnlstilylreyqskvrqifsdvqsevdiynriidel 240

RESULT 6

AA96646

ID MAY96646>standard; Protein; 259 AA.
XX
AC AAY96646;
XX
DT 26-SEP-2000 (first entry)
XX
DE Plant-optimized E. coli heat labile toxin A subunit.
XX
KW Heat-labile toxin; LT-A; LT-B; mutant; transgenic plant; vaccine; oral;
KW adjuvant; anti-bacterial.
XX
OS Escherichia coli.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..18
FT /label= signal_peptide
FT Protein 19..259
FT /label= mature_protein
XX
XX WO200037609-A2.
XX
XX 29-JUN-2000.
XX
XX 22-DEC-1999; 99WO-US30747.
XX
XX 22-DEC-1998; 98US-0113507.
XX
XX (BOYC-) BOYCE THOMPSON INST PLANT RES.
XX (MASO/) MASON H S.
XX (ARNT/) ARNTZEN C J.
XX
XX Mason HS, Arntzen CJ;
XX
XX WPI; 2000-442653/38.
XX N-PSDB; AAA51106.
XX
XX New polynucleotides encoding LT-A or CT-A polypeptides for the
PT transformation of plant cells, useful in immunogenic compositions to
PT elicit immune responses in animals
XX
XX Example 1; Fig 1; 103pp; English.
XX
XX This synthetic Escherichia coli heat-labile toxin (LT) A subunit (LT-A)
CC is encoded by a plant-codon optimized cDNA. The cDNA sequence contains
CC plant-preferred codons and eliminates sequence motifs associated with
CC spurious mRNA processing. A single codon insertion (GTG encoding valine)
CC was made to accommodate the creation of a NcoI restriction site around the
CC initiator methionine codon. Novel polynucleotides encode a mutant LT-A
CC polypeptide or a mutant Vibrio cholerae toxin (CT) A subunit
CC (CT-A) polypeptide, which have reduced enzyme activity as compared to the
CC wild-type LT-A or CT-A polypeptide and where at least one of the codons
CC is altered to a plant preferred codon. The polynucleotide further
CC comprises a nucleic acid sequence encoding LT B subunit (LT-B) or a CT B
CC subunit (CT-B). The polynucleotides are useful for the transformation of
CC plant cells for the production of transgenic plants to produce edible
CC vaccines, especially oral vaccines in transgenic plants for the
CC prophylactic or therapeutic treatment against E. coli or V. cholerae. The
CC mutant polypeptides are also useful as adjuvants.
XX
XX Sequence 259 AA;
SQ

Query Match 98.7%; Score 1287; DB 21; Length 259;
Best Local Similarity 98.3%; Pred. No. 1.7e-125;
Matches 236; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 NGDRLYRADSRPDEIKRSGLMPRGHNEYFDRTGTMNINLYDHARGTGTGFVRYDDGYV 60
Db 20 ngdklyradsrppdeikrsgglmpgrhneyfdrgtgmninlydhargtgtgfvyddgyv 79
QY 61 STSLSLRSAHLAQSGILSGYSTYIIYVIATAPNMENVDVLGVYSPHPYEQEVSALGGIP 120
Db 61 stslsrsahlrgqslsgystyiyviatapnmfndvlgvysphpyeqkvsa199lp 120

Db 80 stslslrsahlagqslgystylyviatapnmfnvndvlgvysphpyeqevsalggip 139
Qy 121 YSQIYGWYRVNFGVTDRLHRNREYDRYRNLTAPAEADGYRLAGFPDHOAWREEPWI 180
Db 140 ysqlygywrvnfgvtdrlhrnreydrfyrnlnlapeadgyrlagfppdhqawreepw1 199
Qy 181 HHAPGCGNSRRTTGTCNEETQNLSTIYLREYOSKVKRQIFSDYQSEVDIYNRIDEL 240
Db 200 hhapggcgdsrtrttgdcneetqnlstlylrkygskvrqifsdysqevdlynrinel 259

RESULT 7
ID AAY96647 standard; Protein: 259 AA.
XX AAY96647;
XX 26-SEP-2000 (first entry)
XX Synthetic E. coli LT-A K63 mutant.
XX Heat-labile toxin; LT-A; LT-B; mutein; transgenic plant; vaccine; oral;
KW adjuvant; anti-bacterial; S63k.
XX Escherichia coli.
OS Synthetic.
XX Key Location/Qualifiers
FH Peptide 1..19
FT /label= signal_peptide
FT /note= "20"
FT Protein 20..259
FT /label= mature_protein
FT Misc-difference 82
FT /label= S63K
FT /note= "Wild-type serine is replaced by lysine"
XX
XX WO200037609-A2.
XX 29-JUN-2000.
XX 22-DEC-1999; 99WO-US30747.
XX 22-DEC-1998; 98US-0113507.
XX (BOYC-) BOYCE THOMPSON INST PLANT RES.
PA (MASO/) MASON H S.
PA (ARNT/) ARNTZEN C J.
XX Mason HS, Arntzen CJ;
XX WPI: 2000-442653/38.
XX N-PSDB: AAA51147.
XX New polynucleotides encoding LT-A or CT-A polypeptides for the
PT transformation of plant cells, useful in immunogenic compositions to
PT elicit immune responses in animals
XX
XX Example 2; Page -: 103pp; English.

This is mutant S63K Escherichia coli heat-labile toxin (LT) A subunit (LT-A). The wild-type serine was replaced with lysine at residue 63 of the mature protein, which was caused by a codon change of TCC to AAG in the coding sequence. The sequence contains plant-preferred codons and eliminates sequence motifs associated with spurious mRNA processing. A single codon insertion (GTG encoding valine) was made to accommodate the creation of a NcoI restriction site around the initiator methionine codon. Novel polynucleotides encode a mutant LT-A polypeptide or a mutant Vibrio cholerae cholera toxin (CT) A subunit (CT-A) polypeptide, which have reduced enzyme activity as compared to the wild-type LT-A or CT-A polypeptide and where at least one of the codons is altered to a plant preferred codon. The polynucleotide further comprises a nucleic acid sequence encoding LT B subunit (LT-B) or a CT B subunit (CT-B). The

CC polynucleotides are useful for the transformation of plant cells for the
CC production of transgenic plants to produce edible vaccines, especially
CC oral vaccines in transgenic plants for the prophylactic or therapeutic
CC treatment against E. coli or V. cholerae. The mutant polypeptides are
CC also useful as adjuvants.
CC NB: This sequence does not appear in the specification, it was made from
CC the wild type sequence shown in AAY96647, which appears in Figure 1.
XX
SQ Sequence 259 AA;

Query Match 98.4%; Score 1283; DB 21; Length 259;
Best Local Similarity 97.9%; Pred. No. 4.5e-125;
Matches 235; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
Qy 1 NGDRLYRADSRPPDEIKRSGGLMPRGHNEYFDRTQMNNINLYDHARGTGTGFVYDDGYV 60
Db 20 ngdklyradsrppdeikrsgglmpgrhneyfdrgtqmnninlydhargtgtgfvryddgyv 79
Qy 61 STSLSLRSALHAGOSILSGYSTYIYVIATAPNMFNVDVLGVSYPHPEQEVSAALGGIP 120
Db 80 stklslrsahlagqslgystylyviatapnmfnvndvlgvysphpyeqevsalggip 139
Qy 121 YSQIYGWYRVNFGVTDRLHRNREYDRYRNLTAPAEADGYRLAGFPDHOAWREEPWI 180
Db 140 ysqlygywrvnfgvtdrlhrnreydrfyrnlnlapeadgyrlagfppdhqawreepw1 199
Qy 181 HHAPGCGNSRRTTGTCNEETQNLSTIYLREYOSKVKRQIFSDYQSEVDIYNRIDEL 240
Db 200 hhapggcgdsrtrttgdcneetqnlstlylrkygskvrqifsdysqevdlynrinel 259

RESULT 8
ID AAY96649 standard; Protein: 259 AA.
XX AAY96649;
XX 26-SEP-2000 (first entry)
XX Plant-optimized E. coli LT-A R72 mutant.
XX Heat-labile toxin; LT-A; LT-B; mutant; transgenic plant; vaccine; oral;
KW adjuvant; anti-bacterial; A72R.
XX Escherichia coli.
OS Synthetic.
XX Key Location/Qualifiers
FH Peptide 1..19
FT /label= signal_peptide
FT Protein 20..259
FT /label= mature_protein
FT Misc-difference 91
FT /label= A72R
FT /note= "Wild type alanine is replaced by arginine"
XX
XX WO200037609-A2.
XX 29-JUN-2000.
XX 22-DEC-1999; 99WO-US30747.
XX 22-DEC-1998; 98US-0113507.
XX (BOYC-) BOYCE THOMPSON INST PLANT RES.
PA (MASO/) MASON H S.
PA (ARNT/) ARNTZEN C J.
XX Mason HS, Arntzen CJ;
XX WPI: 2000-442653/38.
XX N-PSDB: AAA51545.

XX New polynucleotides encoding LT-A or CT-A polypeptides for the
PT transformation of plant cells, useful in immunogenic compositions to
PT elicit immune responses in animals
XX
PS Example 4; Page -; 103pp; English.
XX
CC This is mutant A72R Escherichia coli heat-labile toxin (LT) A subunit
CC (LT-A). The wild-type alanine was replaced with arginine at residue 72
CC of the mature protein, which was caused by a nucleotide change of GC to
CC AG at position 273-274 in the coding sequence. The sequence contains
CC plant-preferred codons and eliminates sequence motifs associated with
CC spurious mRNA processing. A single codon insertion (GTG encoding valine)
CC was made to accommodate the creation of a NcoI restriction site around
CC the initiator methionine codon. Novel polynucleotides encode a mutant
CC LT-A polypeptide or a mutant Vibrio cholerae cholera toxin (CT) A
CC subunit (CT-A) polypeptide, which have reduced enzyme activity as
CC compared to the wild-type LT-A or CT-A polypeptide and where at least one
CC of the codons is altered to a plant preferred codon. The polynucleotide
CC further comprises a nucleic acid sequence encoding LT B subunit (LT-B) or
CC a CT B subunit (CT-B). The polynucleotides are useful for the
CC transformation of plant cells for the production of transgenic plants to
CC produce edible vaccines, especially oral vaccines in transgenic plants
CC for the prophylactic or therapeutic treatment against E. coli or V.
CC cholerae. The mutant polypeptides are also useful as adjuvants.
CC Note: This sequence does not appear in the specification. It was
CC constructed from the wild type LT-A shown in AAY96646 which is given
CC in Figure 1 of the specification.
XX
SQ Sequence 259 AA;

Query Match 98.3%; Score 1282; DB 21; Length 259;
Best Local Similarity 97.9%; Pred. No. 5.7e-125;
Matches 235; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 NGDRLYRADSRPDEIKRSGGLMPRGHNEYFDRGTQMINLYDHARGTGTGFVRYDDGYV 60
Db 20 ngdklyradsrppdeikrsgglmprgnhneyfdrtgqmnlnlydhargtgtgtfryddgyv 79
QY 61 STSLSRSAHLAQSLSGYSTYIYVVIATAPNMNNDVLGVYSPHPYEQEVSALGGIP 120
Db 80 stslsrslrshlraqslsgystyiyviatapnmfnvndvlgvysphpyeqevsalggip 139
QY 121 YSQIYGWYRVNFGVIDERLHNRREYDRYRNLIAPAEDGYRLAGFPDPHQAWREEPWI 180
Db 140 ysqiygywrvnfgviderlhrnreaydrdryrnlniapaedgyrlagfpdpdqawreepwi 199
QY 181 HHAPOCGNSRRTTGTCTNEETQNLSTIYLYREYQSKVKRQIFSDYQSEVDIYNRIDEL 240
Db 200 hhapqcgdsrsrttgdctneetqnlstlylrkyqskvkrqifsdysqsevdynrlnel 259

RESULT 9
AAY96648
ID AAY96648 standard; Protein; 259 AA.
XX
AC AAY96648;
XX
DT 26-SEP-2000 (first entry)
XX
DE Plant-optimized E. coli LT-A G192 mutant.
XX
KW Heat-labile toxin; LT-A; LT-B; mutant; transgenic plant; vaccine; oral;
KW adjuvant; anti-bacterial; R192G.
XX
OS Escherichia coli.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= signal_peptide
FT Protein 20..259

FT Misc-difference 211 /label= mature_protein
FT FT /label= R192G
FT FT /note= "Wild-type arginine is replaced by glycine"
XX
PN WO200037609-A2.
XX
PD 29-JUN-2000.
XX
PF 22-DEC-1999; 99WO-US30747.
XX
PR 22-DEC-1998; 98US-0113507.
XX
PA (BOYC-) BOYCE THOMPSON INST PLANT RES.
PA (MASO/) MASON H S.
PA (ARNT/) ARNTZEN C J.
XX
PI Mason HS, Arntzen CJ;
XX
DR WPI; 2000-442653/38.
DR N-PSDB; AAA51544.
XX
PT New polynucleotides encoding LT-A or CT-A polypeptides for the
PT transformation of plant cells, useful in immunogenic compositions to
PT elicit immune responses in animals
XX
PS Example 3; Page -; 103pp; English.
XX
CC This is mutant R192G Escherichia coli heat-labile toxin (LT) A subunit
CC (LT-A). The wild-type arginine was replaced with glycine at residue 192
CC of the mature protein, which was caused by a codon change of TCC to AAG
CC in the coding sequence. The sequence contains plant-preferred codons and
CC eliminates sequence motifs associated with spurious mRNA processing. A
CC single codon insertion (GTG encoding valine) was made to accommodate the
CC creation of a NcoI restriction site around the initiator methionine
CC codon. Novel polynucleotides encode a mutant LT-A polypeptide or a
CC mutant Vibrio cholerae cholera toxin (CT) A subunit (CT-A) polypeptide,
CC which have reduced enzyme activity as compared to the wild-type LT-A or
CC CT-A polypeptide and where at least one of the codons is altered to a
CC plant preferred codon. The polynucleotide further comprises a nucleic
CC acid sequence encoding LT B subunit (LT-B) or a CT B subunit (CT-B). The
CC polynucleotides are useful for the transformation of plant cells for the
CC production of transgenic plants to produce edible vaccines, especially
CC oral vaccines in transgenic plants for the prophylactic or therapeutic
CC treatment against E. coli or V. cholerae. The mutant polypeptides are
CC also useful as adjuvants.
CC NB: This sequence does not appear in the specification, it was made from
CC the wild type sequence shown in AAY96647, which appears in Figure 1.
XX
SQ Sequence 259 AA;

Query Match 98.2%; Score 1280; DB 21; Length 259;
Best Local Similarity 97.9%; Pred. No. 9.3e-125;
Matches 235; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 NGDRLYRADSRPDEIKRSGGLMPRGHNEYFDRGTQMINLYDHARGTGTGFVRYDDGYV 60
Db 20 ngdklyradsrppdeikrsgglmprgnhneyfdrtgqmnlnlydhargtgtgtfryddgyv 79
QY 61 STSLSRSAHLAQSLSGYSTYIYVVIATAPNMNNDVLGVYSPHPYEQEVSALGGIP 120
Db 80 stslsrslrshlraqslsgystyiyviatapnmfnvndvlgvysphpyeqevsalggip 139
QY 121 YSQIYGWYRVNFGVIDERLHNRREYDRYRNLIAPAEDGYRLAGFPDPHQAWREEPWI 180
Db 140 ysqiygywrvnfgviderlhrnreaydrdryrnlniapaedgyrlagfpdpdqawreepwi 199
QY 181 HHAPOCGNSRRTTGTCTNEETQNLSTIYLYREYQSKVKRQIFSDYQSEVDIYNRIDEL 240
Db 200 hhapqcgdsrsrttgdctneetqnlstlylrkyqskvkrqifsdysqsevdynrlnel 259

RESULT 10
AAU00507
ID AAU00507 standard; Protein; 380 AA.
XX
AC AAU00507;
XX
XX 29-AUG-2001 (first entry)
XX
DE E. coli heat-labile enterotoxin (LT) mutant LTdel110/112.
XX
XX Heat-labile enterotoxin; LT; LTS63Y; LTdel110/112; mutant;
KW detoxified and immunologically active protein; ADP-ribosylation; Gs;
KW endotoxin; diarrhoea; mutein.
XX
OS Escherichia coli strain K88ac.
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT MISC_feature 7
FT MISC_feature /note= "Important residue for enzymatic activity"
FT MISC_feature 44
FT MISC_feature /note= "Important residue for enzymatic activity"
FT Region 58..72
FT /note= "Forms the NAD-binding site"
FT MISC_feature 61
FT MISC_feature /note= "Important residue for enzymatic activity"
FT MISC-difference 257
FT /note= "Encoded by TG"
XX
XX WO200119998-A1.
XX
XX 22-MAR-2001.
PD
XX 15-SEP-1999; 99WO-KR00555.
PF
XX 15-SEP-1999; 99WO-KR00555.
PR
XX (MOGA-) MOGAM BIOTECHNOLOGY RES INST.
PA
XX Park EJ, Kim JS, Chang J, Yum J, Chung S;
XX WPI: 2001-281524/29.
XX N-PSDB; AAS01506.
DR
XX New detoxified mutants of Escherichia coli heat-labile enterotoxin
PT useful as vaccine for preventing and treating diarrhoea, and as adjuvant
PT for antibody production
XX
XX Claim 6; Page 42-44; 48pp; English.
XX
XX The present sequence represents Escherichia coli heat-labile
CC enterotoxin (LT) mutant LTdel110/112. LTS63Y (AAU00506) and LTdel110/112
CC are two novel detoxified and immunologically active proteins (LT
CC mutants) derived by site-directed mutagenesis of the A1 subunit of wild
CC type LT. The substitution of Ser to Tyr at position 63 in LTS63Y blocks
CC NAD-binding. Deletion of Glu residues at positions 110 and 112 in
CC LTdel110/112 eliminate the enzymatic activity of LT. The A1 subunit of
CC wild type LT catalyses ADP-ribosylation of Gs, a GTP-binding protein that
CC regulates CAMP levels. The resulting increase in CAMP is the cause of
CC diarrhoea in humans and animals e.g. pigs. The mucosal immunogenicities
CC of mutant heat-labile endotoxins LTS63Y and LTdel110/112 were tested.
CC Groups of mice were immunised with LTS623Y or LTdel110/112. The control
CC groups received phosphate buffered saline (PBS) alone. The serum and
CC faecal antibody titres to LT were determined. The results showed that
CC mice immunised with LTS63Y or LTdel110/112 contained high and
CC comparable level of anti-LT antibodies in sera and faecal extracts
CC compared with those immunised with wild-type LT. The LT mutants are
CC useful as a vaccine for preventing and treating diarrhoea and as an
CC adjuvant for antibody production.
XX
XX Sequence 380 AA;

Query Match 98.2%; Score 1280; DB 22; Length 380;
Best Local Similarity 98.8%; Pred. No. 1.6e-124;
Matches 237; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
QY 1 NGDRLYRADSRPPDEIKRSGGLMPRGHNEVFDRGTQNNINLYDHARTGTQTGFVRYDDGYV 60
DB 19 ngdrlYradsrppdeikrsgglmpRGHNEVFDRGTQNNINLYDHARTGTQTGFVRYDDGYV 78
QY 61 STSLSLRSALHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVSPHPYEQEVSALGGIP 120
DB 79 stslslrsahlagqsilsgystyyiYVIATAPNMFNVNDVLGVSPHPY--qvsalggip 136
QY 121 YSQIYGYWRVNFVIDERLHNRREYRDYRYNENIATPAEDGYRLAGPPDHQAWRESPWI 180
DB 137 ysqIygywrvnfgvIderlhrnreYrdryrYnlnIaPaedgyrIagfpdDhqawreSpwi 196
QY 181 HHAPOGCGNSRRTITGTCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIDEL 240
DB 197 hhapogcgnsrTITGTCneetqnlstIylreYqskvkrqIfsdyqsevdIynrIdel 256
RESULT 11
AAU96650
ID AAY96650 standard; Protein; 259 AA.
XX
AC AAY96650;
XX
XX 26-SEP-2000 (first entry)
XX
XX Plant-optimized E. coli LT-A A63K+R192G mutant.
XX
XX Heat-labile toxin; LT-A; LT-B; mutant; transgenic plant; vaccine; oral;
KW adjuvant; anti-bacterial; A63K+R192G; double mutein.
XX
XX Escherichia coli.
OS
XX Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= signal_peptide
FT Protein 20..259
FT /label= mature_protein
FT MISC-difference 82
FT /label= S63K
FT /note= "the wild type serine is replaced by lysine
FT at position 63 of the mature sequence"
FT MISC-difference 211
FT /label= R192G
FT /note= "the wild type arginine is replaced by glycine
FT at position 192 of the mature sequence"
XX
XX WO200037609-A2.
XX
XX 29-JUN-2000.
XX
XX 22-DEC-1999; 99WO-US30747.
XX
XX 22-DEC-1998; 98US-0113507.
XX
XX (BOYC-) BOYCE THOMPSON INST PLANT RES.
XX (NASO/) MASON H S.
XX (ARNT/) ARNTZEN C J.
XX
XX Mason HS, Arntzen CJ;
XX WPI: 2000-442653/38.
XX
XX New polynucleotides encoding LT-A or CT-A polypeptides for the
PT transformation of plant cells, useful in immunogenic compositions to
PT elicit immune responses in animals
XX
XX Example 5; Page -; 103pp; English.
XX

ID AAW67772 standard; Protein; 237 AA.
XX AAW67772;
AC
XX
DT 11-MAY-1999 (first entry)
XX
DE E. coli heat labile toxin.
XX
KW A subunit; heat labile toxin; ADP-ribosylation; mutant; detoxification;
KW parenteral adjuvant; antigen; antigen; immunisation; humoral response;
KW cell-mediated immune response; virus; bacterium; parasite; fungus;
KW tumour; allergen; pathogen; AIDS; autoimmune disease; cancer; antibody;
KW systemic lupus erythematosus; Alzheimer's disease; diagnosis.
XX
OS Escherichia coli.
XX
PN WO9842375-A1.
XX
PD 01-OCT-1998.
XX
XX 19-MAR-1998; 98WO-0505454.
XX
PR 18-MAR-1998; 98US-0044696.
PR 21-MAR-1997; 97US-0041227.
XX
PA (CHIR) CHIRON CORP.
XX
XX Barchfeld G, Del Giudice G, Rappuoli R;
XX WPI; 1999-070064/06.
DR N-PSDB; AAV81595.
XX
PT Detoxified mutants of bacterial ADP-ribosylating toxins as
PT parenteral adjuvants - useful to enhance humoral and cell-mediated
PT immune responses in vertebrates when administered with selected
PT antigen e.g. in disease treatment
XX
PS Disclosure; Fig 1A-B; 51pp; English.
XX
CC This sequence corresponds to the amino acid sequence of the A subunit of
CC the E. coli heat labile toxin, an example of a bacterial ADP-ribosylating
CC toxin. A mutant detoxified form of this protein is used in a parenteral
CC adjuvant composition, which comprises the detoxified protein, at least
CC one selected antigen and optionally a pharmaceutically acceptable
CC (optionally topical) vehicle. The adjuvant composition can be
CC administered parenterally in conjunction with at least one antigen in
CC methods to immunise vertebrate subjects. The adjuvant has the ability
CC to enhance the humoral and cell-mediated immune responses elicited by
CC the antigen (e.g. by making the antigen more strongly immunogenic or
CC necessitating fewer/lower antigen doses). It can be administered
CC prior/subsequent to the antigen, and is preferably administered within
CC a short space of time to the same site; it can also be administered in
CC isolation from antigens as a boost following systemic or mucosal antigen
CC administration. Most preferably, the adjuvant is co-administered with
CC the antigen in the compositions and a pharmaceutically acceptable
CC carrier. The antigen may be derived from viruses, bacteria, parasites
CC and fungi or may be tumour antigens, self-antigens and allergens. The
CC compositions are therefore useful in the treatment and prevention of
CC e.g. viral diseases, allergic manifestations, diseases caused by
CC pathogens (e.g. bacteria or parasites), AIDS, autoimmune diseases
CC (e.g. Systemic Lupus Erythematosus), Alzheimer's disease and cancers.
CC The adjuvant can also be used to prepare antibodies against selected
CC antigen(s), useful e.g. for diagnostic purposes or for antigen
CC purification.
XX
SQ Sequence 237 AA;

Query Match 91.3%; Score 1190.5; DB 20; Length 237;
Best Local Similarity 92.9%; Pred. No. 1.7e-115;
Matches 223; Conservative 3; Mismatches 11; Indels 3; Gaps 1;
QY 1 NGDRLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQNNINLYDHARTQTGFVRYDDGYV 60

Db 1 NGDRLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQNNINLYDHARTQTGFVRYDDGYV 60
QY 61 STSLSLRSAHLAGOSILSGYSTYIYVIATAPNMFNVDVLGVSPHPYEQEVSALGGIP 120
Db 61 STSLSLRSAHLAGOSILSGYSTYIYVIATAPNMFNVDVLGVSPHPYEQEVSALGGIP 117
QY 121 YSQIYGYRVNFGVIDERLHRNREYRDYRNINLPAEDGYRLAGFPDPHQAWREEPWI 180
Db 118 YSQIYGYRVNFGVIDERLHRNREYRDYRNINLPAEDGYRLAGFPDPHQAWREEPWI 177
QY 181 HHAPQCGNSRRITGTCNEETQNLSTIYLREYQSKVKQIFSDYQSEVDIYNRIDEL 240
Db 178 HHAPQCGNSRRITGTCNEETQNLSTIYLREYQSKVKQIFSDYQSEVDIYNRIDEL 237

RESULT 14
AAR38728
ID AAR38728 standard; Protein; 236 AA.
XX
AC AAR38728;
XX
DT 08-DEC-1993 (first entry)
XX
DE E.coli heat labile toxin subunit A.
XX
KW enterotoxigenic bacteria; vaccine; immunogenic detoxified LT-A;
KW protomer A; site-directed mutagenesis; reduced toxicity;
KW ADP-ribosyltransferase activity.
XX
OS Escherichia coli.
XX
PN WO9313202-A.
XX
PD 08-JUL-1993.
XX
XX 30-DEC-1992; 92WO-EP03016.
XX
XX 31-DEC-1991; 91IT-OMI3513.
XX (BIOC-) BIOGINE SCLAVO SPA.
XX Domenighini M, Hol W, Pizza M, Rappuoli R;
XX WPI; 1993-227320/28.
DR N-PSDB; AAQ42768.
XX
PT Immunogenic detoxified mutant cholera toxin and heat labile toxin
PT - useful as vaccines against infection by Vibrio cholerae and
PT enterotoxin producing Escherichia coli
XX
PS Disclosure; Fig 2; 60pp; English.
XX
CC This is the sequence of the A subunit of the heat labile toxin (LT-A)
CC of a strain of E.coli known to affect humans. The sequence was
CC published by Yamamoto et al, J.Biol. Chem., 259, 5037-5044.
CC Mutations at selected positions within this sequence have been found
CC to reduce toxicity (see AAR38730-R38732 and AAR44016-R44025). The
CC invention relates to such immunogenic, detoxified proteins and their
CC use in vaccines to protect against enterotoxigenic E.coli.
XX
SQ Sequence 236 AA;

Query Match 90.7%; Score 1183; DB 14; Length 236;
Best Local Similarity 93.3%; Pred. No. 1e-114;
Matches 224; Conservative 2; Mismatches 10; Indels 4; Gaps 2;
QY 1 NGDRLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQNNINLYDHARTQTGFVRYDDGYV 60
Db 1 NGDRLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQNNINLYDHARTQTGFVRYDDGYV 59
QY 61 STSLSLRSAHLAGOSILSGYSTYIYVIATAPNMFNVDVLGVSPHPYEQEVSALGGIP 120

Db 60 stslsrsahlagqylsgysltiyvia---nmfnvndvisvysphpyeqeysalggip 116
 QY 121 YSQIYGYRVNFGVIDERLHNRNREYRDYRNINIAPAEDGYRLAGFPDPDQAWREEPWI 180
 Db 117 ysqlygyrvnfgviderlhrnreayrdyrynlniapaedgyrlagfpdqawreepwi 176
 QY 181 HHAPQGCNSRTITGTCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL 240
 Db 177 hhapqgcgsdrtitgdtcneetqnlstlylreygskvkrqifsdysqvsevdynrirdel 236

RESULT 15

AAU14105
 ID AAU14105 standard; peptide; 254 AA.

XX AC AAU14105;

XX 21-NOV-2001 (first entry)

XX Peptide sequence from Escherichia coli heat labile enterotoxin A.

XX Anti-retroviral; DP178-like; DP107-like; heat labile enterotoxin A;
 KW antifusogenic; antiviral; HIV transmission.

XX Escherichia coli.

XX WO200151673-A2.

XX 19-JUL-2001.

XX 05-JUL-2000; 2000WO-US35727.

XX 09-JUL-1999; 99US-0350841.

XX (TRIM-) TRIMERIS INC.

XX Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;
 PI WPI; 2001-442157/47.

XX

XX Identifying a compound that inhibits the formation of or disrupts a
 PT DP107/DP178 complex, especially compounds with antifusogenic, antiviral
 PT or intracellular modulatory activity, by detecting the formation of a
 PT DP107/DP178 complex -

XX Disclosure; Fig 43; 259pp; English.

XX The present invention relates to peptides which exhibit anti-retroviral
 CC activity. The peptides of the invention (AAU12559-AAU14009) comprise
 CC DP178-like and DP107-like peptides. The DP178 peptide corresponds
 CC to amino acids 639-673 of the transmembrane protein gp41 from human
 CC immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide
 CC corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention
 CC also relates to a method of identifying compounds that inhibit the
 CC formation of or disrupts a DP107/DP178 complex. The method comprises
 CC detecting the formation of a DP107/DP178 complex, both in the presence
 CC or absence of a test compound, in a reaction mixture containing DP107
 CC and DP178 peptides. The method is useful for identifying compounds,
 CC including small molecule compounds, which may themselves exhibit
 CC antifusogenic, antiviral or intracellular modulatory activity. The
 CC DP178-like/DP107-like peptides are useful to inhibit human and non-human
 CC retroviral, particularly HIV, transmission to uninfected cells. The
 CC present sequence represents a peptide sequence from Escherichia coli
 CC heat labile enterotoxin A.

XX Sequence 254 AA;

Query Match

Best Local Similarity 93.3%; Score 1183; DB 22; Length 254;

Matches 224; Conservative 2; Mismatches 10; Indels 4; Gaps 2;

QY * 1 NGDHLRADSRPPDEIKRSGLMPRGHNEYFDRCGTQNMNINLYDHARTGTGTFVRYDDGYV 60
 Db 19 ngdrlradsrppdpdeikrfrslmprg-neyfdrgtqnmnlnlydhargtqtgfvryddgyv 77
 QY 61 STSLSLSAHLAGOSILSGYSTYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIP 120
 Db 78 stslsrsahlagqylsgysltiyvia---nmfnvndvisvysphpyeqeysalggip 134
 QY 121 YSQIYGYRVNFGVIDERLHNRNREYRDYRNINIAPAEDGYRLAGFPDPDQAWREEPWI 180
 Db 135 ysqlygyrvnfgviderlhrnreayrdyrynlniapaedgyrlagfpdqawreepwi 194
 QY 181 HHAPQGCNSRTITGTCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL 240
 Db 195 hhapqgcgsdrtitgdtcneetqnlstlylreygskvkrqifsdysqvsevdynrirdel 254

Search completed: June 10, 2002, 17:31:46
 Job time: 1053 sec

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OM protein - protein search, using sw model

Run on: June 10, 2002, 17:29:43 ; Search time 19.04 Seconds
(without alignments)
1211.210 Million cell updates/sec

Title: US-09-297-171-1
Perfect score: 1304
Sequence: 1 NGDRLYRADSRPPDEIKRSG.....QIFSDYQSEVDIYNIRDEL 240

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1287	98.7	258	1 QLECA	heat-labile entero
2	1088	83.4	258	1 XVVCA	cholera enterotoxi
3	679.5	52.1	259	2 A29831	heat-labile entero
4	394.5	30.3	125	2 A61345	heat-labile entero
5	152	11.7	46	2 S39239	cholera enterotoxi
6	96	7.4	269	1 B25973	pertussis toxin ch
7	93	7.1	268	1 WEBR11	pertussis toxin ch
8	93	7.1	269	1 WEBR1P	pertussis toxin ch
9	91.5	7.0	472	1 A47402	fatty acid binding
10	91	7.0	392	2 T01849	hypothetical prote
11	90.5	6.9	702	2 A61619	arylphorin precurs
12	88.5	6.8	332	2 S60935	hypothetical prote
13	88	6.7	269	1 A25973	pertussis toxin ch
14	88	6.7	547	2 T43666	hypothetical prote
15	87	6.7	809	2 T40574	guanine nucleotide
16	86.5	6.6	145	2 G81094	hypothetical prote
17	86.5	6.6	566	2 A48860	beta-glucosidase,
18	86	6.6	423	2 A72616	probable glutamate
19	85.5	6.6	435	2 E72563	probable tRNA nucl
20	83.5	6.4	870	2 S27514	mosquitocidal toxi
21	83	6.4	254	2 A34759	prion protein - Ch
22	83	6.4	254	2 B34759	prion protein - go
23	83	6.4	353	2 F96903	hypothetical prote
24	83	6.4	7829	2 T15789	hypothetical prote
25	82	6.3	256	2 JU0268	major prion protei
26	82	6.3	446	1 S74920	imu protein - syne
27	82	6.3	469	1 S77704	6-phosphofructo-2-
28	82	6.3	471	1 K1RTFB	6-phosphofructo-2-
29	81.5	6.2	828	1 D39142	outer membrane ush

30	81	6.2	264	2 A54330	major prion protei
31	81	6.2	899	2 B38529	nikB protein - Esc
32	80.5	6.2	173	2 T41773	LEF-6 orf28 - Bomb
33	80.5	6.2	252	2 E71704	hypothetical prote
34	80.5	6.2	880	2 S60137	beta-N-acetylhexos
35	80	6.1	254	1 UJHVIH	major prion PrP-Sc
36	80	6.1	257	2 A23545	major prion PrP27-
37	80	6.1	260	2 S53629	major prion protei
38	80	6.1	264	2 S37137	prion protein - gr
39	80	6.1	3972	2 S75251	hypothetical prote
40	79	6.1	474	2 S16250	phytoene dehydroge
41	79	6.1	509	2 AD0649	probable secreted
42	79	6.1	630	2 A86389	70-3K hypothetical
43	78.5	6.0	648	2 S10869	enterotoxin A - Cl
44	78.5	6.0	767	2 T43398	SCF complex protei
45	78.5	6.0	983	2 H72510	probable ribonucle

ALIGNMENTS

RESULT 1

QLECA

heat-labile enterotoxin A precursor - Escherichia coli

C.Species: Escherichia coli

C.Date: 30-Apr-1981 #sequence_revision 17-Oct-1997 #text_change 18-Jun-1999

C.Accession: I55231; A01817; A26946

R.Yamamoto, T.; Tamura, T.; Yokota, T.

J. Biol. Chem. 259, 5037-5044, 1984

A.Title: Primary structure of heat-labile enterotoxin produced by Escherichia coli pa

A.Reference number: I55231; MUID:84185610

A.Accession: I55231

A.Status: preliminary; translated from GB/EMBL/DDBJ

A.Molecule type: DNA

A.Residues: 1-258 <RES>

A.Cross-references: GB:K01995; NID:g148027; PIDN:AAA24685.1; PID:g148028

R.Spicer, E.K.; Noble, J.A.

J. Biol. Chem. 257, 5716-5721, 1982

A.Title: Escherichia coli heat-labile enterotoxin. Nucleotide sequence of the A subun

A.Reference number: A01817; MUID:82167425

A.Accession: A01817

A.Molecule type: DNA

A.Residues: 1-21, 'R', '23-36, 'FRS', '40-44, 46-92, 'Y', '94-99, 'LTIYI', '105-107, 111-118, 'IS', '1

A.Cross-references: EMBL:V00275; NID:g41339; PIDN:CAA23532.1; PID:g41340

A.Note: the authors translated the codon TAT for residue 93 as Ser

R.Yamamoto, T.; Gojobori, T.; Yokota, T.

J. Bacteriol. 169, 1352-1357, 1987

A.Title: Evolutionary origin of pathogenic determinants in enterotoxigenic Escherichi

A.Reference number: A26946; MUID:87137303

A.Accession: A26946

A.Molecule type: DNA

A.Residues: 1-21, 'R', '23-206, 'N', '208-230, 'E', '232-255, 'D', '257-258 <YAM>

A.Cross-references: EMBL:M15363

C.Comment: The heat-labile enterotoxin molecule contains one A chain and five or six

C.Genetics:

A.Gene: elta

C.Superfamily: heat-labile enterotoxin chain A

C.Keywords: enterotoxin

F:1-18/Domain: signal sequence #status predicted <SIG>

F:19-258/Product: heat-labile enterotoxin chain A #status predicted <MAT>

Query Match 98.7%; Score 1287; DB 1; Length 258;

Best Local Similarity 98.3%; Pred. No. 1.3e-110;

Matches 236; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 NGDRLYRADSRPPDEIKRSGGLMPRGHNEVFDRTGTMNINLYDHARTGTGFGVYDDGYV 60

Db 19 NGDRLYRADSRPPDEIKRSGGLMPRGHNEVFDRTGTMNINLYDHARTGTGFGVYDDGYV 78

QY 61 STSLSRSLRAGOSILSGYSTYIYVIATAPNMFNVNDVLGVYSPRPYBOEYSALGGIP 120

Db 79 STSLRSALHAQGSILSGYSTIYIVATAPNMFNVNDVLGVSPHPYEQEVSALGGIP 138

QY 121 YSQIYGWYRVNFGVIDERLHNRNREYDRYRNLIAPAEDGYRLAGFPDPHQAWREEPWI 180
|||||

Db 139 YSQIYGWYRVNFGVIDERLHNRNREYDRYRNLIAPAEDGYRLAGFPDPHQAWREEPWI 198
|||||

QY 181 HHAPOGCGNSRRTITGDTCTNEETONLSTIYLRYSQSKVRQIFSDYQSEVDIYNRIRDEL 240
|||||

Db 199 HHAPOGCGDSRRTITGDTCTNEETONLSTIYLRYSQSKVRQIFSDYQSEVDIYNRIRDEL 258
|||||

RESULT 2

XVUCA
Cholera enterotoxin chain A precursor VCL1457 [validated] - Vibrio cholerae
C:Species: Vibrio cholerae
C:Date: 06-Jul-1982 #sequence_revision 26-Jan-1996 #text_change 01-Sep-2000
A:Accession: A05129; S14623; S14625; A91268; A91286; A91746; A92298; S17665; B43864; A82
R:Wekalanos, J.J.; Swartz, D.J.; Pearson, G.D.N.; Harford, N.; Groyne, F.; de Wilde, M.
Nature 306, 551-557, 1983
A:Reference number: A93320; MUID:84068199
A:Accession: A05129
A:Molecule type: DNA
A:Residues: 1-258 <MEK>
R:Dams, E.; de Wolf, M.; Dierick, W.
submitted to the EMBL Data Library, March 1991
A:Description: Correction of the cholera toxin nucleotide sequence of the Vibrio cholera
A:Reference number: S14623
A:Accession: S14623
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-258 <DAL>
A:Cross-references: EMBL:X58786; NID:g48420; PIDN:CAA41592.1; PID:g48421
A:Experimental source: strain 2125
A:Accession: S14625
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-258 <DA2>
A:Cross-references: EMBL:X58785; NID:g48888; PIDN:CAA41590.1; PID:g48889
A:Experimental source: strain 569B
R:Lai, C.Y.; Cancedda, F.; Chang, D.
FEBS Lett. 100, 85-89, 1979
A:Title: Primary structure of cholera toxin subunit A-1. Isolation, partial sequences an
A:Reference number: A91268; MUID:79169830
A:Accession: A91268
A:Molecule type: protein
A:Residues: 37-38,'L',40-44,'SE',47-49,'B',51-55,'B',57,'B',59-60,'B',62-66,'Z',68-72,'I
R:Duffy, L.K.; Peterson, J.W.; Kurosky, A.
FEBS Lett. 126, 187-190, 1981
A:Title: Isolation and characterization of a precursor form of the 'A' subunit of cholera
A:Reference number: A91286; MUID:81212799
A:Accession: A91286
A:Molecule type: protein
A:Residues: 19,'N',21-27 <DUF>
R:Klapper, D.G.; Finkelstein, R.A.; Capra, J.D.
Immunochimistry 13, 603-611, 1976
A:Title: Subunit structure and N-terminal amino acid sequence of the three chains of cho
A:Reference number: A91746; MUID:76259136
A:Accession: A91746
A:Molecule type: protein
A:Residues: 19-36,'R',38,213-232 <KLA>
R:Duffy, L.K.; Peterson, J.W.; Kurosky, A.
J. Biol. Chem. 256, 12252-12256, 1981
A:Title: Covalent structure of the gamma chain of the A subunit of cholera toxin.
A:Reference number: A92298; MUID:82053094
A:Accession: A92298
A:Molecule type: protein
A:Residues: 213-246,'ID',249-255,'N',257-258 <DU2>
R:Dams, E.; de Wolf, M.; Dierick, W.
Biochim. Biophys. Acta 1090, 139-141, 1991
A:Title: Nucleotide sequence analysis of the CT operon of the Vibrio cholerae classical
A:Reference number: S17665; MUID:91355224
A:Accession: S17665
A>Status: preliminary

A:Molecule type: DNA
A:Residues: 1-258 <DAM>
A:Cross-references: EMBL:X58785; NID:g48888; PIDN:CAA41590.1; PID:g48889
R:Baudry, B.; Tasano, A.; Kettle, J.; Kaper, J.B.
Infect. Immun. 60, 428-434, 1992
A:Title: Cloning of a gene (zot) encoding a new toxin produced by Vibrio cholerae.
A:Reference number: A43864; MUID:92112300
A:Accession: B43864
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-6 <BAU>
A:Cross-references: GB:M83563; NID:gl55314; PIDN:AAA27583.1; PID:gl55316
A:Note: sequence extracted from NCBI backbone (NCBIN:77488, NCBIP:77496)
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers
L. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833
A:Accession: A82197
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-258 <HEI>
A:Cross-references: GB:AE004224; GB:AE003852; NID:g9655952; PIDN:AAF94614.1; GSPDB:GN
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VCL1457
A:Map position: 1
C:Complex: the cholera enterotoxin molecule contains three kinds of chains; an alpha
ciate noncovalently with the subunit B, an aggregate of five beta chains
C:Function:
A:Description: the active component of the toxin that is primarily responsible for s
.2.5) activity also activates intracellular adenylyl cyclase
C:Superfamily: heat-labile enterotoxin chain A
C:Keywords: enterotoxin
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-212/Product: cholera enterotoxin alpha chain #status experimental <CTA>
F:213-256/Product: cholera enterotoxin gamma chain #status experimental <CTG>
F:217/Disulfide bonds: Interchain (to alpha chain) #status predicted

Query Match 83.4%; Score 1088; DB 1; Length 258;
Best Local Similarity 81.7%; Pred. NO. 2.4e-92;
Matches 196; Conservative 24; Mismatches 20; Indels 0; Gaps 0;

QY 1 NGDRLYRADSRPDEIKRSGGLMPRGHNEYFDRTGTMNINLYDHARGTQTGFVRYDDGVV 60
|||||

Db 19 NDDKLYRADSRPDEIKRSGGLMPRGQSEYFDRTGTMNINLYDHARGTQTGFVRYDDGVV 78
|||||

QY 61 STSLRSALHAQGSILSGYSTIYIVATAPNMFNVNDVLGVSPHPYEQEVSALGGIP 120
|||||

Db 79 STSLRSALHAQGSILSGYSTIYIVATAPNMFNVNDVLGVSPHPYEQEVSALGGIP 138
|||||

QY 121 YSQIYGWYRVNFGVIDERLHNRNREYDRYRNLIAPAEDGYRLAGFPDPHQAWREEPWI 180
|||||

Db 139 YSQIYGWYRVNFGVIDERLHNRNREYDRYRNLIAPAEDGYRLAGFPDPHQAWREEPWI 198
|||||

QY 181 HHAPOGCGNSRRTITGDTCTNEETONLSTIYLRYSQSKVRQIFSDYQSEVDIYNRIRDEL 240
|||||

Db 199 HHAPOGCGNSRRTITGDTCTNEETONLSTIYLRYSQSKVRQIFSDYQSEVDIYNRIRDEL 258
|||||

RESULT 3

A29831
heat-labile enterotoxin IIA chain A precursor - Escherichia coli
N:Alternate names: Lt-IIa
C:Species: Escherichia coli
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jul-1999
A:Accession: A29831
R:Pickett, C.L.; Weinstein, D.L.; Holmes, R.K.
J. Bacteriol. 169, 5180-5187, 1987
A:Title: Genetics of type IIA heat-labile enterotoxin of Escherichia coli: operon fus
A:Reference number: A91849; MUID:88032841

A;Accession: A29831
A;Molecule type: DNA
A;Residues: 1-259 <PIC>
A;Cross-references: GB:M17894; NID:g146671; PIDN:AAA24093.1; PID:g146672
A;Note: the authors translated the codon TAT for residue 225 as Thr
C;Superfamily: heat-labile enterotoxin chain A
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-259/Product: heat-labile enterotoxin Iia chain A #status predicted <LTA>

Query Match 52.1%; Score 679.5; DB 2; Length 259;
Best Local Similarity 54.6%; Pred. No. 8.2e-55;
Matches 130; Conservative 39; Mismatches 66; Indels 3; Gaps 2;

QY 6 YRADSRPPDEIKRSGGLMPRGHNEYFDRGTOMNINLYDHARGTGTGFVRDGDGYVSTLS 65
DB 22 FRADSRPPDEIRAGGLPRGQOAYERTPINLYEHARGTGTGNTRYNDGYVSTVT 81

QY 66 LRSALAGQSILSGSYTYIYVIATAPNMFVNDVGLVSPHPYEQEVSALGGIPYSQIY 125
DB 82 LRQAHLLGQNLGSGSYTYIYVAPNLFVDVGLVSPHPYSENEFAALGGIPLSQII 141

QY 126 GWYRVNGVIDERLHNRNRYDRYRNLTAPADGYRLAGFPDPHQAWEERPWIHAPQ 185
DB 142 GWYRVSGAIEGGQMRDYGDLFRGLTVAPNEDGYQLAGFSPNFPAPWEMPWSTAPE 201

QY 186 GCGNSRTITGDCNEETQNLSTIYLREYQSKVKROI-FSDYQSEVDI--YNRIRDEL 240
DB 202 QCVPNNREFGGVCISATNVLSKYDLNFKLLKRRLLATFFNSEDDFIGVHGERDEL 259

RESULT 4
A61345
heat-labile enterotoxin A chain precursor - Escherichia coli (fragments)
C;Species: Escherichia coli
C;Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 17-Mar-1999
R;Spicer, E.K.; Kavanaugh, W.M.; Dallas, W.S.; Falkow, S.; Konigsberg, W.H.; Schafer, D.
C;Accession: A61345
Proc. Natl. Acad. Sci. U.S.A. 78, 50-54, 1981
A;Title: Sequence homologies between a subunits of Escherichia coli and Vibrio cholerae
A;Reference number: A61345; MUID:81223767
A;Accession: A61345
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-125 <SPI>
A;Cross-references: GB:K00433
A;Note: authors translated the codon GAG for residue 27 as Asp, CAA for residue 53 as Glu
C;Superfamily: heat-labile enterotoxin chain A

Query Match 30.3%; Score 394.5; DB 2; Length 125;
Best Local Similarity 39.9%; Pred. No. 4.7e-29;
Matches 87; Conservative 2; Mismatches 6; Indels 123; Gaps 2;

QY 1 NGBRLRADSRPPDEIKRSGGLMPRGHNEYFDRGTOMNINLYDHARGTGTGFVRDGDYV 60
DB 19 NGBRLRAESRPPDEIKRFRSLPRG-NEYFDRGTOMNINLYDHARGTGTGFVR----- 71

QY 61 STSLSLSAHLAQSIILSGSYTYIYVIATAPNMFVNDVGLVSPHPYEQEVSALGGIP 120
DB 72 ----- 71

QY 121 YSQIYGWYRVNGVIDERLHNRNRYDRYRNLTAPADGYRLAGFPDPHQAWEERPWI 180
DB 72 -----RTWI 75

QY 181 HHAQQCGNSRRTITGDCNEETQNLSTIYLREYQSKV 218
DB 76 HHAQQCGDSRRTITGDCNEETQNLSTIYLREYQSKV 113

RESULT 5
S39239

cholera enterotoxin chain A2 - Vibrio cholerae (serotype 0139)
N;Alternate names: CTX2 cholera toxin chain A2
C;Species: Vibrio cholerae
A;Variety: serotype 0139
C;Date: 08-May-1995 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C;Accession: S39239; S39240
R;Lebens, M.; Holmgren, J.
submitted to the EMBL Data Library, November 1993
A;Description: Structure and arrangement of the Cholera toxin genes in vibrio Cholera
A;Reference number: S39238
A;Accession: S39239
A;Molecule type: DNA
A;Residues: 1-46 <LEP>
A;Cross-references: EMBL:X76390; NID:g433856; PIDN:CAA53974.1; PID:g433858; EMBL:X763
A;Experimental source: strain 4260B; serotype 0139
C;Superfamily: heat-labile enterotoxin chain A

Query Match 11.7%; Score 152; DB 2; Length 46;
Best Local Similarity 63.6%; Pred. No. 2.4e-07;
Matches 28; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 197 DTCNEETQNLSTIYLREYQSKVKROI-FSDYQSEVDIYNRIRDEL 240
DB 3 NTCDEKTSGLGVKFLDEYQSKVKRQYFSGYQSDIDTHNRIRDEL 46

RESULT 6
B25973
pertussis toxin chain S1 precursor - Bordetella parapertussis
C;Species: Bordetella parapertussis
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: B25973
R;Arico, B.; Rappuoli, R.
J. Bacteriol. 169, 2847-2853, 1987
A;Title: Bordetella parapertussis and Bordetella bronchiseptica contain transcription
A;Reference number: A25973; MUID:6722217
A;Accession: B25973
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-269 <ARI>
C;Superfamily: pertussis toxin chain S1

Query Match 7.4%; Score 96; DB 1; Length 269;
Best Local Similarity 24.2%; Pred. No. 0.34; Mismatches 24; Indels 90; Gaps 12;

QY 5 LYRADSRPPDEIKRSGGLMPRGHNEYFDRGTOMNINLYDHARGTGTGFVRDGDGYVSTSL 64
DB 41 VYRYDSRPPEDVFQNGFTAGNND-----NVLEHLTGRSCQVSGSSNAFVSTSS 89

QY 65 SLR-----SAHLAQSIILSGSYTYIYVIATAPNMFVNDVGLVSPHPYE 110
DB 90 SRRYTEVLEHRMOEAVEAERAGRG--TGFIYIYEI-RADNMF----- 131

QY 111 QEVSALGIPYSQIYGWYRVNGVIDERLHNRNRYDRYRNLTAPADGYRLAGFP 168
DB 132 -----YGAASSYF-----EYDTYGDNAGRILAGA-----LATYQ 161

QY 169 PDHQAWEERPWIHAPQCGNSRRT-----ITGDCNEETQNLSTIYLREYQSKVKROI 224
DB 162 SEYLAHRRIP-----PENIRTVRVYHNGITGETTTEYPNL-----RYYSQQTRANTN 210

QY 225 DYQS 228
DB 211 PYTS 214

RESULT 7
WEBRI1
pertussis toxin chain S1 precursor (version 1) - Bordetella pertussis
N;Alternate names: histamine-sensitizing factor; islet-activating protein; leukocytos

N:Contains: NAD+ ADP-ribosyltransferase (EC 2.4.2.30)

C:Species: Bordetella pertussis

C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 24-Sep-1999

C:Accession: A24394

R:Locht, C.; Keith, J.M.

Science 232, 1258-1264, 1986

A:Title: Pertussis toxin gene: nucleotide sequence and genetic organization.

A:Reference number: A94285; MUID:86208173

A:Accession: A24394

A:Molecule type: DNA

A:Residues: 1-268 <LOC>

A:CROSS-references: GB:M13223

C:Comment: Pertussis toxin contains five different chains, S1-S5. These are organized in to the membrane receptors. Dimers of S2-S4 and S3-S4 are held together by S5. The genes to Comment: Pertussis toxin causes irreversible uncoupling of the regulatory GTP-binding protein. The substrates for the ADP-ribosyltransferase activity are the GTP-binding protein. Comment: Pertussis toxin is the major virulence factor of B. pertussis.

C:Comment: See PIR:WEBRIP for version 2 of this sequence.

C:Superfamily: pertussis toxin chain S1

C:Keywords: glycosyltransferase; mitogen; pentosyltransferase; toxin; virulence factor;

F;1-34/Domain: signal sequence #status predicted <SIG>

F;35-268/Product: pertussis toxin chain S1 #status predicted <MAT>

Query Match 7.1%; Score 93; DB 1; Length 268;

Best Local Similarity 24.0%; Pred. No. 0.63;

Matches 53; Conservative 22; Mismatches 62; Indels 84; Gaps 11;

QY 5 LYRADSRPPDEIKRSGGLMPRGHNEYFDRTQMNNINLYDHARGTQTGFVRYDDGYVSTSL 64

Db 41 VYRYSRPPEDVFQNGFTAGNND-----NVLDLTLGRSCQVGSNSAFVSTSS 89

QY 65 SLR-----SAHLGOSILSGYSTYIYIATAPNMFNVNDVLGVSPHYE 110

Db 90 SRRYTEVYLEHRMOWEAEVREG--TGHFYIYEV-RADNMF-----LATYQ 161

QY 111 QEVSALGGIPYSQIYGYRVNFGVIDERLHRNREYDRYRNLN--TAPAEGRVLAGFP 168

Db 132 -----YGAASSYF-----EYDVTYDGNAGRILAGA-----LATYQ 161

QY 169 PDQAWREEPWIHAPOGCGNSRT-----ITGDTCNTEETQN 205

Db 162 SEYLAHRRI-----PENIRRVTRVYHNGITGETTTEYSN 197

RESULT 8

WEBRIP

pertussis toxin chain S1 precursor (version 2) - Bordetella pertussis

N:Alternate names: histamine-sensitizing factor; islet-activating protein; lymphocytosis

N:Contains: NAD+ ADP-ribosyltransferase (EC 2.4.2.30)

C:Species: Bordetella pertussis

C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 24-Sep-1999

C:Accession: A24144; S06588; A36176; S04494

R:Nicoia A.; Perugini, M.; Franzini, C.; Casaglini, M.C.; Borri, M.G.; Antoni, G.; Almon

Proc. Natl. Acad. Sci. U.S.A. 83, 4631-4635, 1986

A:Title: Cloning and sequencing of the pertussis toxin genes: operon structure and gene

A:Reference number: A94104; MUID:86259651

A:Accession: A24144

A:Molecule type: DNA

A:Residues: 1-269 <NC>

A:CROSS-references: GB:M14378; NID:gl44070; PIDN:AAA93980.1; PID:gl44071

R:Loosmore, S.M.; Cunningham, J.D.; Bradley, W.R.; Yao, F.L.; Dekaban, G.A.; Klein, M.H.

Nucleic Acids Res. 17, 8365, 1989

A:Title: A unique sequence of the Bordetella pertussis toxin operon.

A:Reference number: S06588; MUID:90045957

A:Accession: S06588

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-67, 'E', 69-231, 'Y', 233-269 <LOO>

A:CROSS-references: EMBL:X16347; NID:g39769; PIDN:CAA34397.1; PID:g39770

R:Cieplak, W.; Burnette, W.N.; Mar, V.L.; Kaljot, K.T.; Morris, C.F.; Chen, K.K.; Sato,

Proc. Natl. Acad. Sci. U.S.A. 85, 4667-4671, 1988

A:Title: Identification of a region in the S1 subunit of pertussis toxin that is require

A:Reference number: A36176; MUID:88263009

A:Accession: A36176

A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual

A:Molecule type: DNA

A:Residues: 35-64 <CIE>

R:Cockle, S.A.

FEBS Lett. 249, 329-332, 1989

A:Title: Identification of an active-site residue in subunit S1 of pertussis toxin by

A:Reference number: S04494; MUID:89290006

A:Accession: S04494

A:Molecule type: protein

A:Residues: 152-162, 'X', 164-166 <COC>

A:Experimental source: strain 10536

C:Comment: See PIR:WEBRIP for version 1 of this sequence.

C:Superfamily: pertussis toxin chain S1

C:Keywords: glycosyltransferase; mitogen; pentosyltransferase; toxin; virulence facto

F;1-34/Domain: signal sequence #status predicted <SIG>

F;35-269/Product: pertussis toxin chain S1 #status predicted <MAT>

Query Match 7.1%; Score 93; DB 1; Length 269;

Best Local Similarity 24.0%; Pred. No. 0.63;

Matches 53; Conservative 22; Mismatches 62; Indels 84; Gaps 11;

QY 5 LYRADSRPPDEIKRSGGLMPRGHNEYFDRTQMNNINLYDHARGTQTGFVRYDDGYVSTSL 64

Db 41 VYRYSRPPEDVFQNGFTAGNND-----NVLDLTLGRSCQVGSNSAFVSTSS 89

QY 65 SLR-----SAHLGOSILSGYSTYIYIATAPNMFNVNDVLGVSPHYE 110

Db 90 SRRYTEVYLEHRMOWEAEVREG--TGHFYIYEV-RADNMF-----LATYQ 161

QY 111 QEVSALGGIPYSQIYGYRVNFGVIDERLHRNREYDRYRNLN--TAPAEGRVLAGFP 168

Db 132 -----YGAASSYF-----EYDVTYDGNAGRILAGA-----LATYQ 161

QY 169 PDQAWREEPWIHAPOGCGNSRT-----ITGDTCNTEETQN 205

Db 162 SEYLAHRRI-----PENIRRVTRVYHNGITGETTTEYSN 197

RESULT 9

A47402

fatty acid binding/transport protein - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 19-May-1995 #sequence_revision 12-Apr-1996 #text_change 22-Jun-1999

C:Accession: A47402

R:Abumrad, N.A.; El-Maghrabi, M.R.; Amri, E.Z.; Lopez, E.; Grimaldi, P.A.

J. Biol. Chem. 268, 17665-17668, 1993

A:Title: Cloning of a rat adipocyte membrane protein implicated in binding or transpo

A:Reference number: A47402; MUID:93352566

A:Accession: A47402

A:Molecule type: mRNA

A:Residues: 1-472 <ABU>

A:CROSS-references: GB:I19658; NID:g310112; PIDN:AAA02878.1; PID:g310113

C:Superfamily: lysosomal integral membrane protein II

C:Keywords: glycoprotein; transmembrane protein

F;2-6/Domain: intracellular #status predicted <CYT1>

F;7-30/Domain: transmembrane #status predicted <TML>

F;31-439/Domain: extracellular #status predicted <EXT>

F;440-466/Domain: transmembrane #status predicted <TM2>

F;467-472/Domain: intracellular #status predicted <CYT2>

F;79,102,134,205,220,235,247,417/Binding site: carbohydrate (Asn) (covalent) #status

Query Match 7.0%; Score 91.5; DB 1; Length 472;

Best Local Similarity 20.1%; Pred. No. 1.8;

Matches 56; Conservative 39; Mismatches 85; Indels 99; Gaps 12;

QY 2 GDRLYRA-----DSRPPDEIKRSGG---LMPRGHNEYFDRTQMNNINLYDHARGTQTGFVR 54

Db 58 GTTVYRQFVDFQNFEEVAKNSKIKVIQRYTYRVRYLAKE-NITQDPKDSVTSFVQ 116

QY 55 YDGGYVSTSLRSALHAGOSILSGYSTYYIYVIATAPNMFNVNDVLGVYS----- 105
Db 117 PNGAIFPSLSVGT-----NDNTVLNLAAVAAPHIYTNFSVOGVNLNLIKSKSS 168
QY 106 -----PHPYEQEVSALGGIPYSQ-IXGYWRVNFQ-----V 134
Db 169 MFQTRSLKELLNGYKDPFLSLVPPYSTVGVF--YPYNTVDGVYKVSNGKDNISKVAI 226
QY 135 IDE-RLHNRREYDRYRNLIAPAEDGYRLAGFPDPHQAWREEPWIHAPQCGGSSRT 193
Db 227 IDTYKGRNLWSYWCMDIN-----GTDAASFP-----LGEKSR 263
QY 194 ITGDTCTNEETQNLSTIYLREYQSKVKROIQSFSDYQSEVDI 232
Db 264 -----LRFSSDICRSIYAVFESEVNL 285
RESULT 10
T01849
hypothetical protein F9D12.5 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 26-Feb-1999
C:Accession: T01849
R:Murray, J.; Langston, Y.; Ahrens, C.
A:Submitted to the EMBL Data Library, July 1998
A:Description: The sequence of Arabidopsis thaliana F9D12.
A:Reference number: Z1444
A:Accession: T01849
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-392 <MUR>
A:Cross-references: EMBL:AF077407; NID:g3319339; PID:g3319347
C:Genetics:
A:Map position: 4
A:Introns: 36/3; 134/2; 191/1; 283/2; 339/1
A:Note: F9D12.5

Query Match 7.0%; Score 91; DB 2; Length 392;
Best Local Similarity 21.5%; Pred. No. 1.6;
Matches 45; Conservative 44; Mismatches 76; Indels 44; Gaps 12;
QY 29 EYFDRGTQMNIN--LYDHARGTGTGFRYDDGVYSTSLRSALHAGOST--LSGYSTY- 83
Db 162 EYLPGRWEVNDVKLFH-NGKLNKYLAIISDGLKLYNDAKRWGFGQLIPHVFTFYTG 220
QY 84 YIYVIATAPNMFNVNDVLGYSPHPYEQEVSALGGIPYSQIYGYWRVNFQVIDERLHNR 143
Db 221 YI-----EQDIGSFGAEIFIVKPAQOEKVTFISN-PPTNVFTWKILHFSILEDKFYSD 274
QY 144 EY--RDYRYRNLIAPAEDG-----YRLA--GFPDPHQAWREEPWIHAPQCGGSSRTIT 195
Db 275 DFLVEDRYWR-LGFNPKDGGGRPYALPIFLFAQGHKA-----NAVATNT 318
QY 196 GDTCTNEETQNLSTIYLREYQSKVKROIQS 224
Db 319 WGAAN-----LRKNQRSTNHRQIYT 339
RESULT 11
A61619
arylphorin precursor - greater wax moth
N:Alternate names: phenylalanine-rich protein Lhp76
C:Species: Galleria mellonella (greater wax moth)
C>Date: 21-Jul-1995 #sequence_revision 11-Aug-1995 #text_change 24-Sep-1999
C:Accession: A61619
R:Mammel, N.A.; Trevitt, P.M.; Silhacek, D.L.; Kumaran, A.K.
Insect Biochem. Mol. Biol. 22, 333-342, 1992
A:Title: Nucleotide sequence and structure of the arylphorin gene from Galleria mellonella
A:Reference number: A61619
A:Accession: A61619
A:Molecule type: DNA
A:Residues: 1-702 <MEM>

A:Cross-references: GB:M73793; NID:g159077; PIDN:AAA74229.1; PID:g159078
A:Note: In the authors' translation, residue 306-Leu is omitted, residue 317-Asn is d
C:Genetics:
A:Introns: 30/1; 74/3; 352/3; 410/2
A:Note: single copy gene
C:Superfamily: arylphorin
C:Keywords: glycoprotein; hemolymph; storage protein
F:1-16/Domain: signal sequence #status predicted <SIG>
F:211,481/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 6.9%; Score 90.5; DB 2; Length 702;
Best Local Similarity 20.4%; Pred. No. 3.8;
Matches 55; Conservative 37; Mismatches 82; Indels 95; Gaps 12;
QY 5 LYRADSRPPDEIKRSGGLMPRGHN---EYFDRG-----TQMNINLYDHARGTGTG 53
Db 149 IHRADTR-----GIVLPAPYEINPEYFMNSDLKVIQMKGLIIPQEGPYGIL 200
QY 54 RYDDG-YVSTSLRSALHAGOSILS-----GYSTYYIYVIATAPNMFNVNDVLG---- 102
Db 201 SKDNAYFYANYSGPLTYEDNELLSYFIEDIGWNSYYIYFHNRFPFWENGEOGLIGPLKE 260
QY 103 -----VYSPHPYEQEVSALGGIPYSQIYGYWRVNFQVIDERLHNRREYDRY 150
Db 261 RGEIYVYVYQKILARYLERLANGLEIP-----RFNWL-----KYQTSY 303
QY 151 -----RNLNTAPAEDEGYRLAGFPDPHQAWREEPWIHAPQCGGSSRTITGTCNEETQ 205
Db 304 PLLSSYQLPFAQRNDYLA-----SGDNIN-DIQF 333
QY 206 LSTIYLREYQSKVKROIQSFSDYQSEVDIYN 234
Db 334 IDT-YERTFLQLQKQGFQKAYKQEVLDIYN 361
RESULT 12
S60935
hypothetical protein YPL055c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein LPE17c
C:Species: Saccharomyces cerevisiae
C>Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 05-Nov-1999
C:Accession: S60935
R:Winnett, E.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Hall, J.; Storms, R.
submitted to the EMBL Data Library, October 1995
A:Reference number: S60921
A:Accession: S60935
A:Molecule type: DNA
A:Residues: 1-332 <WIN>
A:Cross-references: EMBL:U39205; NID:g1079672; PID:g1079687; GSPDB:GN00016; MIPS:YPL0
C:Genetics:
A:Gene: MIPS:YPL055c
A:Map position: 16L
Query Match 6.8%; Score 88.5; DB 2; Length 332;
Best Local Similarity 19.0%; Pred. No. 2.2;
Matches 60; Conservative 38; Mismatches 94; Indels 123; Gaps 15;
QY 2 GDRLYRADSRPPDE-----IKRS-----GGLMPRGHNEYFDRGTQMNINLYDHARGTGTG 51
Db 6 GNNYSYSTPPRQGGYHHARRSGAGGSYRGGNASY--GARYN--SDYEQPPQEG 60
QY 52 FVR-----YDGGYVST--LSLSAHLAAGQ---SILSGYSTYYIYVIATAPNMFNVNDVL 101
Db 61 DLQGTGAYRYNGYTDTRPYYSANSRHYQAQSPRYNNGTNSYHL-----PQNGSODTN 114
QY 102 G-----VYSPHPYEQEV-----SALGGIP-- 120
Db 115 GRTTSAQEDNDEKRVKSRVYRNQADHPROQPMVSGTSSRNGSSGSSSTSSYNGLPPPP 174
QY 121 -----YSQIYGYWRVNFQVIDERLHNRREYDRYRNLIAPAEDGYRLAGFP 168

Query Match 6.8%; Score 88.5; DB 2; Length 332;
Best Local Similarity 19.0%; Pred. No. 2.2;
Matches 60; Conservative 38; Mismatches 94; Indels 123; Gaps 15;
QY 2 GDRLYRADSRPPDE-----IKRS-----GGLMPRGHNEYFDRGTQMNINLYDHARGTGTG 51
Db 6 GNNYSYSTPPRQGGYHHARRSGAGGSYRGGNASY--GARYN--SDYEQPPQEG 60
QY 52 FVR-----YDGGYVST--LSLSAHLAAGQ---SILSGYSTYYIYVIATAPNMFNVNDVL 101
Db 61 DLQGTGAYRYNGYTDTRPYYSANSRHYQAQSPRYNNGTNSYHL-----PQNGSODTN 114
QY 102 G-----VYSPHPYEQEV-----SALGGIP-- 120
Db 115 GRTTSAQEDNDEKRVKSRVYRNQADHPROQPMVSGTSSRNGSSGSSSTSSYNGLPPPP 174
QY 121 -----YSQIYGYWRVNFQVIDERLHNRREYDRYRNLIAPAEDGYRLAGFP 168

Db 175 PSVSSITNRRSYHSSAVPY-----SSSHYNNYHHRETPTPPPPSGNGYAKGYP 222
Qy 169 PDQAWREEPWIHAPQCGN---SSRITGDTCTNEETQNLSTIYLREYQSKVK----- 219
Db 223 V-----HVPENRNSDSSSVVKKRILDMKDSFFIYLDKFNKVKTNTE 270
Qy 220 -----RQIFSDYOS 228
Db 271 SECEKAREVFKESDS 285

RESULT 13

A25973
pertussis toxin chain S1 precursor - Bordetella bronchiseptica
C:Species: Bordetella bronchiseptica
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A25973
R:Arico, B.; Rappuoli, R.
J. Bacteriol. 169, 2847-2853, 1987
A:Title: Bordetella parapertussis and Bordetella bronchiseptica contain transcriptional
A:Reference number: A25973; MUID:8722217
A:Accession: A25973
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-269 <ARI>
C:Superfamily: pertussis toxin chain S1

Query Match 6.7%; Score 88; DB 1; Length 269;
Best Local Similarity 23.5%; Pred. No. 1.8;
Matches 52; Conservative 23; Mismatches 62; Indels 84; Gaps 11;
Qy 5 LYRADSRPDEIKRSGGLMPRGHNEYFDRTQMNNINLYDHARGTQTGFVRYDDGVSTSL 64
Db 41 VYRDSRPDEDVFON-GFTAWGND-----NVLEHLTGRSCQVGSNSAFVSTSS 89
Qy 65 SLR-----SAHLAQSIILSGYSTYIYVIATAPNMFNVNDVLGVSPHPE 110
Db 90 SRRTEYVLEHRMQEAVEERAGRG--TGHFYGIYIEV-RADNNF----- 131
Qy 111 QEVSALGGIPYSQIYGYWYVNFVGRVDERLHRNREYRDYRNLM--IAPAEQGYRLAGFP 168
Db 132 -----YGAASVE-----EYVDYTDGNAGRILAGA-----LATYQ 161
Qy 169 PDQAWREEPWIHAPQCGNSRT-----ITGDFCNEETON 205
Db 162 SEXLAHRRIP-----PENIRRVTRVYHNGITGETTTEYPN 197

RESULT 14

T46366
hypothetical protein DKFZp434C0118.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C:Accession: T46366
R:Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A:Reference number: Z23031
A:Accession: T46366
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-547 <AAA>
A:Cross-references: EMBL:AL137520
A:Experimental source: adult testis; clone DKFZp434C0118
C:Genetics:
A:Note: DKFZp434C0118.1

Query Match 6.7%; Score 88; DB 2; Length 547;
Best Local Similarity 23.4%; Pred. No. 4.7;
Matches 39; Conservative 32; Mismatches 62; Indels 34; Gaps 9;
Qy 53 VRYDDGVSTSLRSRAHLAQSIILSY-----STYIYVIATAPNMFNVNDVLGVSP 106

Db 364 VRFDGVVTSKTYIRQ---GEQSLDGFYRAWHQVEYYRI-----RFFPDGHVVMLTTP 414
Qy 107 HPYEQEVSAL--GGIPYSQIYGYWYVNF-----FGVIDERL-HRNREYRDYRNLM 153
Db 415 EEPQSIYVPLRNLRTNRDAILLGHYRLSQDQTDNQTQKFAVITKKKEKPLDYKYRFRV 474
Qy 154 NIAPAEQGYR--LAGFPPDQAWREEPWIHAPQCGNSRRTITGDT 198
Db 475 PVQEAQDSFHVGLQLCSSGHQRFNKLIIWHHS---CHITYKS-TGET 517

RESULT 15

T40574
guanine nucleotide binding protein beta subunit-like - fission yeast (Schizosaccharom
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T40574
R:Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, January 1999
A:Reference number: Z21938
A:Accession: T40574
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-809 <SEE>
A:Cross-references: EMBL:AL035226; PIDN:CAA22832.1; GSPDB:GN000067
A:Experimental source: strain 972h-; cosmid c609
C:Genetics:
A:Gene: SPAC609.03
A:Map position: 2
A:Introns: 21/1; 52/2; 280/3; 780/2

Query Match 6.7%; Score 87; DB 2; Length 809;
Best Local Similarity 22.6%; Pred. No. 9.6;
Matches 43; Conservative 29; Mismatches 54; Indels 64; Gaps 12;
Qy 1 NGD---RLYRADSRPDEIKRSGGLMPRGHNEYFDRTQMNNINLYDHARGTQTGFVRYDD 57
Db 110 SGOKLIKLFDLDS-----SKEGGM-----DHGMEQTQRCWSCALDSVKNIIVPCDN 154
Qy 58 GY-----VSTSLSLRSRAHLAGO-----SILSGYSTYI--YVIATAPNMFNVNDVL 101
Db 155 GHTFLVCSEGTARQYDIREPHVCNQDLDCPSILVNTNPNYRNLYTITMSPS----- 206
Qy 102 GVYSPHPYEQEVSALGGI-PYSQIYGYWYVNFVGRVDERLHRNREYRDYRNLMIAPAED 160
Db 207 -----NPY---YFAIGGTHEYAFLY-----DRRMVK-KSFRDDW--TMNTSPEKD 245
Qy 161 GYRLAGFPPD 170
Db 246 CRCVRKFSPPD 255

Search completed: June 10, 2002, 17:32:32
Job time: 169 sec

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	1304	100.0	258	1	ELAP_ECOLI	P06717	escherichia
2	1292	99.1	258	1	ELAH_ECOLI	P04530	escherichia
3	1088	83.4	258	1	CHTA_VIBCH	P01555	vibrio chol
4	682	52.3	263	1	E2BA_ECOLI	P04528	escherichia
5	679.5	52.1	259	1	E2AA_ECOLI	P13810	escherichia
6	93	7.1	269	1	TOXI_BORPE	P04977	bordetella
7	91.5	7.0	471	1	CD36_RAT	Q07969	rattus norv
8	88.5	6.8	566	1	BGLX_MAIZE	P49235	zea mays (m
9	88	6.7	447	1	FBX9_HUMAN	Q9UK97	homo sapien
10	86	6.6	423	1	DHE3_AERPE	Q9YC65	aeropyrum p
11	84.5	6.5	826	1	CRAA_BACUH	Q95597	bacillus th
12	83	6.4	254	1	PRIO_CRIGR	Q60506	cricetulus
13	83	6.4	254	1	PRIO_CHIMI	Q60468	cricetulus
14	82	6.3	256	1	PRE2_BOVIN	Q01880	bos taurus
15	82	6.3	257	1	PRIO_PIG	P49927	sus scrofa
16	82	6.3	446	1	SUN_SYNY3	P72943	synecocyst
17	82	6.3	470	1	F261_RAT	P07953	rattus norv
18	81.5	6.2	419	1	NSMA_MOUSE	O70572	mus musculu
19	81.5	6.2	828	1	MRKC_KLEPN	P21647	klebsiella
20	81	6.2	256	1	PRIO_CEREL	P79142	cervus elap
21	81	6.2	256	1	PRIO_FELCA	O18754	felis silve
22	81	6.2	264	1	PRIO_BOVIN	P10379	bos taurus
23	80.5	6.2	252	1	Y455_RICPR	Q9zd88	ricettsia
24	80.5	6.2	880	1	LYTD_BACSU	P39848	bacillus su
25	80	6.1	254	1	PRIO_MESAU	P04273	mesocricetu
26	80	6.1	256	1	PRE2_TREST	P40243	tragelaphus
27	80	6.1	264	1	PR19_HUMAN	P04242	tragelaphus
28	79.5	6.1	629	1	Z195_HAUST	O14628	homo sapien
29	79	6.1	238	1	PRIO_THEGE	Q95270	theropitheci
30	79	6.1	246	1	PRIO_CERTO	Q95176	cercocebus
31	79	6.1	260	1	PRIO_SAISC	P40258	saimiri sci
32	79	6.1	474	1	CRTI_SYNP7	P26294	synecococci
33	78.5	6.0	255	1	PRIO_CAMDR	P79141	camelus dro

RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RX MEDLINE=91238966; PubMed=2034287;
 RA Sixma T.K., Pronk S.E., Raik K.H., Wartna E.S., van Zanten B.A.M.,
 RA Witholt B., Hol W.G.J.;
 RT "Crystal structure of a cholera toxin-related heat-labile enterotoxin
 RT from *E. coli*.";
 RL Nature 351:371-377(1991).
 RN [8]
 RP DISCUSSION OF SEQUENCE.
 RX MEDLINE=95349400; PubMed=7623669;
 RA Domenighini M., Pizzo M., Jobling M.G., Holmes R.K., Rappuoli R.;
 RT "Identification of errors among database sequence entries and
 RT comparison of correct amino acid sequences for the heat-labile
 RT enterotoxins of *Escherichia coli* and *Vibrio cholerae*.";
 RL Mol. Microbiol. 15:1165-1167(1995).
 CC -!- FUNCTION: THE BIOLOGICAL ACTIVITY OF THE TOXIN IS PRODUCED BY
 CC THE A CHAIN, WHICH ACTIVATES INTRACELLULAR ADENYL CYCLASE.
 CC -!- SUBUNIT: HETEROHEXAMER OF ONE A CHAIN AND OF FIVE B CHAINS.
 CC -----
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 CC -----
 DR EMBL; M15361; AAA24791.1; -;
 DR EMBL; M15362; AAA24793.1; -;
 DR EMBL; M35581; AAA98202.1; -;
 DR EMBL; V00275; CAA23532.1; -;
 DR EMBL; M57244; AAB59161.1; -;
 DR EMBL; M61015; AAA24335.1; -;
 DR EMBL; A04913; CAA00402.1; -;
 DR PIR; A26946; QLECEA.
 DR PIR; A01817; QLECA.
 DR PDB; 1LTA; 31-JAN-94.
 DR PDB; 1LFB; 31-JUL-94.
 DR PDB; 1LFG; 15-SEP-95.
 DR PDB; 1LTI; 17-AUG-96.
 DR PDB; 1LTS; 31-JAN-94.
 DR PDB; 1LTT; 31-JAN-94.
 DR PDB; 1LTJ; 07-JUL-97.
 DR PDB; 1LR4; 16-JUN-97.
 DR PDB; 1LHT; 20-APR-95.
 DR InterPro: IPR001144; Enterotoxin_A.
 DR Pfam: PF01375; Enterotoxin_A; 1.
 DR PRINTS: PR00771; ENTEROTOXINA.
 KW Enterotoxin; Signal; 3D-structure.
 FT SIGNAL 1 18
 FT CHAIN 19 258 HEAT-LABILE ENTEROTOXIN A CHAIN.
 FT DISULFID 205 217
 FT ACT_SITE 130 130
 FT VARIANT 130 130
 FT CONFLICT 37 39 E -> K (IN INACTIVE MUTANT).
 FT CONFLICT 45 45 SGG -> FRS (IN REF. 3).
 FT CONFLICT 93 93 MISSING (IN REF. 3).
 FT CONFLICT 100 110 TYIVYIATAP -> LTIVIVIA (IN REF. 3).
 FT CONFLICT 119 120 LG -> IS (IN REF. 3).
 FT CONFLICT 159 159 R -> G (IN REF. 4).
 FT CONFLICT 207 207 N -> D (IN REF. 3).
 FT STRAND 23 27
 FT HELIX 31 37
 FT TURN 38 38
 FT STRAND 39 40
 FT TURN 43 44
 FT TURN 48 49
 FT HELIX 59 64
 FT TURN 75 76
 FT STRAND 77 81
 FT HELIX 84 95
 FT STRAND 100 106
 FT TURN 110 111

FT	STRAND	112	114
FT	HELIX	115	122
FT	HELIX	126	128
FT	STRAND	130	134
FT	TURN	135	135
FT	STRAND	137	138
FT	HELIX	139	141
FT	STRAND	142	149
FT	TURN	150	151
FT	STRAND	152	153
FT	TURN	158	159
FT	TURN	161	162
FT	HELIX	165	168
FT	TURN	169	170
FT	STRAND	174	174
FT	HELIX	176	178
FT	TURN	179	179
FT	HELIX	180	182
FT	TURN	187	188
FT	HELIX	190	193
FT	TURN	195	196
FT	HELIX	197	200
FT	TURN	203	204
FT	HELIX	215	240
FT	TURN	241	241
FT	HELIX	242	244
FT	HELIX	250	253
SQ	SEQUENCE	258 AA; 29902 MW; 2F0786442619F81F CRC64;	

Query Match 100.0%; Score 1304; DB 1; Length 258;
 Best Local Similarity 100.0%; Pred. No. 1.5e-112;
 Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	NGDRLYRADSRPPDEIKRSGGLMPRGHNEVDRGTOMNINLYDHARGTQTFVRYDDGYV	60
Db	19	NGDRLYRADSRPPDEIKRSGGLMPRGHNEVDRGTOMNINLYDHARGTQTFVRYDDGYV	78
QY	61	STSLSRSAHLAGQSILSGYSTYYIYVIATAPNNFNVDVGLVYSPHPYEQEVSALGGIP	120
Db	79	STSLSRSAHLAGQSILSGYSTYYIYVIATAPNNFNVDVGLVYSPHPYEQEVSALGGIP	138
QY	121	YSOIYGYRVNFGVIDERLHRNREYDRYRNINIAPAEDGYRLAGPPDPHQAWREPWI	180
Db	139	YSOIYGYRVNFGVIDERLHRNREYDRYRNINIAPAEDGYRLAGPPDPHQAWREPWI	198
QY	181	HHAPOCGNSSRTITGDTCTNEETONLSTIYLVREYQSKVKRQIFSDYOSEVDIYNRIDEL	240
Db	199	HHAPOCGNSSRTITGDTCTNEETONLSTIYLVREYQSKVKRQIFSDYOSEVDIYNRIDEL	258

RESULT 2
 ELAHL_ECOLI STANDARD; PRT; 258 AA.
 AC P43530;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Heat-labile enterotoxin A chain precursor (LT-A, human) (LTH-A).
 GN ELTA OR LTFA OR TOXA.
 OS *Escherichia coli*.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC *Escherichia*.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ISOLATE H10407;
 RX MEDLINE=841185610; PubMed=6325417;
 RA Yamamoto T., Tamura T., Yokota T.;
 RT "Primary structure of heat-labile enterotoxin produced by *Escherichia*
 RT *coli* pathogenic for humans.";
 RL J. Biol. Chem. 259:5037-5044(1984).
 RN [2]

```
RP REVISION TO 207.
RC STRAIN=ISOLATE H10407;
RX MEDLINE=87137303; PubMed=3546273;
RA Yamamoto T., Gojobori T., Yokota T.;
RT "Evolutionary origin of pathogenic determinants in enterotoxigenic
RL Escherichia coli and Vibrio cholerae O1.";
RN J. Bacteriol. 169:1352-1357(1987).
[3]
RC SEQUENCE FROM N.A.
RX STRAIN=ISOLATE H10407;
RA MEDLINE=9325225; PubMed=8486242;
RT Inoue T., Tsuji T., Koto M., Imamura S., Miyama A.;
RT "Amino acid sequence of heat-labile enterotoxin from chicken
RT enterotoxigenic Escherichia coli is identical to that of human strain
RT H 10407.";
RN FEMS Microbiol. Lett. 108:157-161(1993).
[4]
RC DISCUSSION OF SEQUENCE.
RX MEDLINE=95349400; PubMed=7623669;
RA Domenighini M., Pizzi M., Jobling M.G., Holmes R.K., Rappuoli R.;
RT "Identification of errors among database sequence entries and
RT comparison of correct amino acid sequences for the heat-labile
RT enterotoxins of Escherichia coli and Vibrio cholerae.";
RL Mol. Microbiol. 15:1165-1167(1995).
CC -1- FUNCTION: THE BIOLOGICAL ACTIVITY OF THE TOXIN IS PRODUCED BY
CC THE A CHAIN, WHICH ACTIVATES INTRACELLULAR ADENYL CYCLASE.
CC -1- SUBUNIT: HETEROHEXAMER OF ONE A CHAIN AND OF FIVE B CHAINS.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; K01995; AAA24685.1; -.
DR EMBL; S60731; CAB31891.1; -.
DR HSPF; P06717.1; ITG.
DR InterPro; IPR001144; Enterotoxin_A.
DR Pfam; PF01375; Enterotoxin_A; 1.
DR PRINTS; PR00771; ENTEROTOXINA.
KW Enterotoxin; Signal.
FT SIGNAL 1 18 BY SIMILARITY.
FT CHAIN 19 258 HEAT-LABILE ENTEROTOXIN A CHAIN.
FT DISULFID 205 217 BY SIMILARITY.
FT ACT_SITE 128 128 BY SIMILARITY.
FT CONFLICT 207 207 N -> D (IN REF. 1 AND 3).
SQ SEQUENCE 258 AA; 29872 MW; 2BB153C777FD78B7 CRC64;

Query Match 99.1%; Score 1292; DB 1; Length 258;
Best Local Similarity 98.8%; Pred. No. 1.9e-111;
Matches 237; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 NGDRLYRADSRPPDIKRSGLGMPGHNEYFDRTGTMNINLYDHARGTQTFVRYDDGVV 60
Db 19 NGDKLYRADSRPPDIKRSGLGMPGHNEYFDRTGTMNINLYDHARGTQTFVRYDDGVV 78
QY 61 STLSLSRSLAHLAGQSILSGSYTYTYVVTATAPNMNVNDVLGVSPHPYEQEVSALGGIP 120
Db 79 STLSLSRSLAHLAGQSILSGSYTYTYVVTATAPNMNVNDVLGVSPHPYEQEVSALGGIP 138
QY 121 YSQIYGVYRVNFGVIDERLHRRNREYRDYRNLNLTAPADGDYVLGFPDPHQAREEPWI 180
Db 139 YSQIYGVYRVNFGVIDERLHRRNREYRDYRNLNLTAPADGDYVLGFPDPHQAREEPWI 198
QY 181 HHAPOCGNSSRTITGDCNEETQNLSTLYLREYQSKVKRQIFSDYQSEVDIYNIRDEL 240
Db 199 HHAPOCGNSSRTITGDCNEETQNLSTLYLREYQSKVKRQIFSDYQSEVDIYNIRDEL 258

RESULT 3
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CHTA_VIBCH STANDARD; PRT; 258 AA.
AC P01555; Q56634; Q9JVPV1;
DT 21-JUL-1986 (Rel. 01, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cholera enterotoxin, A chain precursor (NAD(+)-diphthamide ADP-
DE ribosyltransferase) (EC 2.4.2.36) (Cholera enterotoxin A subunit).
GN CXTA OR TOXA OR VC1457.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EL TOR 2125;
RX MEDLINE=84068199; PubMed=6646234;
RA Mekalanos J.J., Swartz D.J., Pearson G.D.N., Harford N., Groyne F.,
RA de Wilde M.;
RT "Cholera toxin genes: nucleotide sequence, deletion analysis and
RT vaccine development.";
RL Nature 306:551-557(1983).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CLASSICAL 569B / ATCC 25870 / SEROTYPE O1;
RX MEDLINE=91355224; PubMed=1883840;
RA Dams E., de Wolf M., Dierick W.;
RT "Nucleotide sequence analysis of the CT operon of the Vibrio cholerae
RT classical strain 569B.";
RL Biochim. Biophys. Acta 1090:139-141(1991).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=1854 / O139-BENGAL;
RA Yamamoto K., Do V.G.R.F., Xu M., Iida T., Miwatani T., Albert M.J.,
RA Honda T.;
RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=EL TOR 2125;
RA Dams E., de Wolf M., Dierick W.;
RL Submitted (MAY-1991) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=KNIH002;
RA Shin H.J., Park Y.C., Kim Y.C.;
RT "Cloning and nucleotide sequence analysis of the virulence gene
RT cassette from Vibrio cholerae KNIH002 isolated in Korea.";
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=EL TOR N16961 / SEROTYPE O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae.";
RL Nature 406:477-483(2000).
RN [7]
RP SEQUENCE OF 1-212 FROM N.A.
RC STRAIN=CLASSICAL 569B / ATCC 25870 / SEROTYPE O1;
RX MEDLINE=85006737; PubMed=6090390;
RA Lockman H.A., Galen J.E., Kaper J.B.;
RT "Vibrio cholerae enterotoxin genes: nucleotide sequence analysis of
RT DNA encoding ADP-ribosyltransferase.";
RL J. Bacteriol. 159:1086-1089(1984).
RN [8]
RP SEQUENCE OF 213-258 FROM N.A.
RX MEDLINE=84061784; PubMed=6315707;
RA Lockman H., Kaper J.B.;
```

RT "Nucleotide sequence analysis of the A2 and B subunits of Vibrio
 RL cholerae enterotoxin.",
 RA J. Biol. Chem. 258:13722-13726(1983).
 RP [9]
 RP SEQUENCE OF 19-27.
 RX MEDLINE=81212799; PubMed=7238869;
 RA Duffy L.K., Peterson J.W., Kurosky A.;
 RT "Isolation and characterization of a precursor form of the 'A'
 RL subunit of cholera toxin.",
 RL FEBS Lett. 126:187-190(1981).
 RN [10]
 RP SEQUENCE OF 19-38 AND 213-232.
 RX MEDLINE=76259136; PubMed=955672;
 RA Klapper D.G., Finkelstein R.A., Capra J.D.;
 RT "Subunit structure and N-terminal amino acid sequence of the three
 RL chains of cholera enterotoxin.",
 RL Immunochimistry 13:605-611(1976).
 RN [11]
 RP SEQUENCE OF 27-72 AND 111-139.
 RX MEDLINE=79169830; PubMed=437113;
 RA Lai C.-Y., Cancedda F., Chang D.;
 RT "Primary structure of cholera toxin subunit A1: isolation, partial
 RL sequences and alignment of the BrCN fragments.",
 RL FEBS Lett. 100:85-89(1979).
 RN [12]
 RP SEQUENCE OF 213-258.
 RX MEDLINE=82053094; PubMed=7028752;
 RA Duffy L.K., Peterson J.W., Kurosky A.;
 RT "Covalent structure of the gamma chain of the A subunit of cholera
 RL toxin.",
 RL J. Biol. Chem. 256:12252-12256(1981).
 RN [13]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
 RX MEDLINE=95387395; PubMed=7658473;
 RA Zhang R.G., Scott D.L., Westbrook M.L., Nance S., Spangler B.D.,
 RA Shipley G.G., Westbrook E.M.;
 RT "The three-dimensional crystal structure of cholera toxin.",
 RL J. Mol. Biol. 251:563-573(1995).
 CC -!- FUNCTION: THE ALPHA/GAMMA CHAIN (A SUBUNIT) IS AN ADP-RIBOSYLATING
 CC TOXIN.
 CC -!- CATALYTIC ACTIVITY: NAD(+) + peptide diphthamide = nicotinamide +
 CC peptide N-(ADP-D-ribosyl)diphthamide.
 CC -!- SUBUNIT: CONTAINS 3 KINDS OF CHAINS, AN ALPHA AND A GAMMA CHAIN
 CC (FROM THE SAME PRECURSOR MOLECULE), LINKED BY AN INTERCHAIN
 CC DISULFIDE BOND, ASSOCIATE NONCOVALENTLY WITH AN AGGREGATE OF 4 TO
 CC 6 BETA CHAINS.
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 CC -----
 DR EMBL; X00171; CAA24995.1; -;
 DR EMBL; X58785; CAA1590.1; -;
 DR EMBL; D30053; BAA06290.1; -;
 DR EMBL; X58786; CAA41592.1; -;
 DR EMBL; K02679; AAA27514.1; -;
 DR EMBL; AF175708; AAD51359.1; -;
 DR EMBL; AE004224; AAF94614.1; -;
 DR EMBL; K01170; AAA27572.1; -;
 DR EMBL; D30052; BAA06288.1; -;
 DR PIR; A01818; XVCA. -;
 DR PIR; A05129; A05129. -;
 DR PIR; S14625; S14625. -;
 DR PIR; S17665; S17665. -;
 DR PIR; S14623; S14623. -;
 DR PDB; 1XPB; 01-APR-97. -;
 DR PDB; 1ATC; 01-AUG-96. -;
 DR TIGR; VC1457; -;
 DR InterPro; IPR001144; Enterotoxin_A.

DR Pfam; PF01375; Enterotoxin_A; 1.
 DR PRINTS; PR00771; ENTEROTOXIN.
 KW Enterotoxin; Signal; NAD; Transferase; Glycosyltransferase;
 KW 3D-structure; Complete proteome.
 FT SIGNAL 1 18
 FT CHAIN 19 212 CHOLERA ENTEROTOXIN, CHAIN-A1 (ALPHA).
 FT CHAIN 213 258 CHOLERA ENTEROTOXIN, CHAIN-A2 (GAMMA).
 FT DISULFID 217 217 INTERCHAIN (WITH GAMMA CHAIN).
 FT ACT_SITE 62 62 INTERACT WITH NAD (BY SIMILARITY).
 FT ACT_SITE 130 130 BY SIMILARITY.
 FT CONFLICT 20 20 D -> N (IN REF. 9).
 FT CONFLICT 37 37 S -> R (IN REF. 10).
 FT CONFLICT 39 39 G -> L (IN REF. 11).
 FT CONFLICT 45 46 QS -> SE (IN REF. 11).
 FT CONFLICT 111 111 N -> L (IN REF. 11).
 FT CONFLICT 132 132 S -> A (IN REF. 11).
 FT CONFLICT 213 213 M -> I (IN REF. 1).
 FT CONFLICT 247 248 DI -> ID (IN REF. 12).
 FT CONFLICT 256 256 D -> N (IN REF. 12).
 SQ SEQUENCE 258 AA; 29335 MW; 0F7EBAE62069A5D0 CRC64;

Query Match 83.4%; Score 1088; DB 1; Length 258;
 Best Local Similarity 81.7%; Pred. No. 1e-92;

Matches 196; Conservative 24; Mismatches 20; Indels 0; Gaps 0;

QY 1 NGRRLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTOMNINLYDHARGTQTGTVRYDGGYV 60
 Db 19 NDDKLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTOMNINLYDHARGTQTGTVRYDGGYV 78
 QY 61 STSLSLSAHLAQOSILSGSYTYVIYVATAPNMFNNDVLGVSPHPYEQEVSALGGIP 120
 Db 79 STSLSLSAHLVGTILSGHSTYVIYVATAPNMFNNDVLGVSPHPYEQEVSALGGIP 138
 QY 121 YSQIYGHYRVNFGVIDERLHNRNRYDRYRNLAIAEDGYRLAGPPDQHQAREPWI 180
 Db 139 YSQIYGHYRVHFGVLDQLHNRNRYDRYRNLAIAEDGYRLAGPPDQHQAREPWI 198
 QY 181 HHAPQCGNSRRTTGTCNEETONLSTIYLYREYQSKVKRQIFSDYQSEVDIYNRIDEL 240
 Db 199 HHAPQCGNAPRSMSTNCTDEKTSGLGVKFLDEIQSKVKRQIFSGYQSDIDTHNRKDEL 258

RESULT 4
 E2BA_ECOLI STANDARD; PRT; 263 AA.
 AC P43528;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Heat-labile enterotoxin IIB, A chain precursor (LT-IIB).
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=ISOLATE 41;
 RX MEDLINE=89359131; PubMed=2670900;
 RA Pickett C.L., Twiddy E.M., Coker C., Holmes R.K.;
 RT "Cloning, nucleotide sequence, and hybridization studies of the type
 RL IIB heat-labile enterotoxin gene of Escherichia coli.",
 RL J. Bacteriol. 171:4945-4952(1989).
 RN [2]
 RN X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS).
 RX MEDLINE=96399713; PubMed=8805549;
 RA van den Akker F., Sarfaty S., Twiddy E.M., Connell T.D., Holmes R.K.,
 RA Hol W.G.;
 RT "Crystal structure of a new heat-labile enterotoxin, LT-IIB.",
 RL Structure 4:665-678(1996).
 CC -!- FUNCTION: THE BIOLOGICAL ACTIVITY OF THE TOXIN IS PRODUCED BY
 CC THE A CHAIN, WHICH ACTIVATES INTRACELLULAR ADENYL CYCLASE.
 CC -!- SUBUNIT: HETEROHEXAMER OF ONE A CHAIN AND OF FIVE B CHAINS.

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CC -----
CC EMBL; M28523; AAA53285.1; -.
CC PDB; 1TII; PRELIMINARY.
CC InterPro; IPR001144; Enterotoxin_A.
CC Pfam; PF01375; Enterotoxin_A; 1.
CC PRINTS; PR00771; ENTEROTOXINA.
CC Enterotoxin; Signal; 3D-structure.
CC FT SIGNAL 1 20
CC FT CHAIN 21 263 HEAT-LABILE ENTEROTOXIN IIB, A CHAIN.
CC FT DISULFID 205 217
CC FT ACT_SITE 130 130
CC SEQUENCE 263 AA; 29485 MW; A56E8A069427CFB9 CRC64;
CC -----
Query Match 52.3%; Score 682; DB 1; Length 263;
Best Local Similarity. 57.4%; Pred. No. 1.9e-55;
Matches 124; Conservative 35; Mismatches 57; Indels 0; Gaps 0;
CC QY 6 YRDSRPDEIKRSGGLMPRGHNEYFDGQTOMINLYDHARGTGTGFRVYDDGYVSTLS 65
CC Db :||||| :||||| :||| : :||| :||||| :||| :||| :||| :||| :
CC 24 FRADSRTPDEVRSSGLIPRGQDEAYERGTPININLYDHARGTATGNTRYNDGYVSTTTT 83
CC QY 66 LRSAHLAGQSILSGSYIIYIVTATAPNMVNVDVLGVYSPHPYEQEVSALGGTIPYSQIY 125
CC Db ||||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
CC 84 LRQAHLLGQNMGLGYNYYIYVAAAPNLFDVNGVLGGRYSPYSPSENYAALGGIPLSQII 143
CC QY 126 GWYRVNFGVIDERLHRNREYRDYRNLNLTAPADGGYRLAGFPDHOAWREEPWIHAQP 185
CC Db ||||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
CC 144 GWYRVSGATGGWHRNDRYRDLFRGLSAPNEDGVRGIAGFPDGFPAWEVPPWREFAPN 203
CC QY 186 GCGNSSRTITGTCNEETONLSTIYLREYQSKVKRQ 221
CC Db |::: ||| ||| ||| :||| :||| :||| :||| :||| :||| :|||
CC 204 SCLPNPKASSDPTTCASLTNKLQSHDLADFKKYIKRK 239
CC -----
RESULT 5
E2AA_ECOLI ID E2AA_ECOLI STANDARD; PRT; 259 AA.
AC P13810;
AT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Heat-labile enterotoxin IIA, A chain precursor (LT-IIA).
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
ON [1]
ON SEQUENCE FROM N.A.
RP MEDLINE=88032841; PubMed=2822667;
RA Pickett C.L., Weinstein D.L., Holmes R.K.;
RT "Genetics of type IIA heat-labile enterotoxin of Escherichia coli:
RT operon fusions, nucleotide sequence, and hybridization studies.";
RL J. Bacteriol. 169:5180-5187(1987).
CC -!- FUNCTION: THE BIOLOGICAL ACTIVITY OF THE TOXIN IS PRODUCED BY
CC THE A CHAIN, WHICH ACTIVATES INTRACELLULAR ADENYL CYCLASE.
CC -!- SUBUNIT: HETEROHEXAMER OF ONE A CHAIN AND OF FIVE B CHAINS.
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CC EMBL; M17894; AAA24093.1; -.
DR PIR; A29831; A29831.
DR HSSP; P43528; 1TII.
DR InterPro; IPR001144; Enterotoxin_A.
DR Pfam; PF01375; Enterotoxin_A, 1.
DR PRINTS; PR00771; ENTEROTOXINA.
DR Enterotoxin; Signal.
KW SIGNAL 1 18
FT CHAIN 19 259 HEAT-LABILE ENTEROTOXIN IIA, A CHAIN.
FT DISULFID 203 215 BY SIMILARITY.
FT ACT_SITE 128 128 BY SIMILARITY.
SQ SEQUENCE 259 AA; 29242 MW; 996F31IA32CABEA CRC64;

Query Match 52.1%; Score 679.5; DB 1; Length 259;
Best Local Similarity 54.6%; Pred. No. 3.2e-55;
Matches 130; Conservative 39; Mismatches 66; Indels 3; Gaps 2;

QY 6 YRADSRPDEIKRSGMLPRGHNEYFDQGTOMNINLYDHARGTGTGPRVYDDGVYVTSLS 65
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
22 FRADSRTPDEIRAGGLPRGOEAYERGTPINILYEHARGTGTGNTRYNDGVYVTSVT 81
QY 66 LRSALHAGQSITLSCYSTSYIYVITATAMFNENVNDVLGVYSPHPYEQEVSALGGIPYSQIY 125
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
82 LRQALHLGQNILGSNEYIYVAPAPNLFDVNGVLGRYSPYPSENFEEFALGGIPLSQII 141
QY 126 GWYRVNFGVIDERLHRNREYRDYRYRNLTAPADGYRLAGFPDHOAWREEPWIHAPO 185
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
142 GWYVSGALTEGGQMQRNDRYDGLFRGLTVPANEDGYQLAGFPNFPAWREMPHSTAPE 201
QY 186 GCGNSRTITGDCNTEQNTQNLSTIYLYREYQSKVKRQI-FSDYQSEVDI--YNRIRDEL 240
Db :||:| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
202 QCVPNKKEFGGVGCISATNVLSKYDLNFKLLKRLALTFMSEDDDFIGVHGERDEL 259

RESULT 6
TOX1_BORPE STANDARD; PRT; 269 AA.
ID TOX1_BORPE AC P04977;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DE Pertussis toxin subunit 1 precursor (PTX S1) (Islet-activating protein
GN S1) (IAP S1) (NAD-dependent ADP-ribosyltransferase (EC 2.4.2.-)).
OS Bordetella pertussis.
OC Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
OC Bordetella.
OX NCBI_TaxID=520;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BP165;
RX MEDLINE=862359651; PubMed=2873570;
RA Nicosia A., Perugini M., Franzini C., Casagli M.C., Borri M.G.,
RA Antoni G., Almonni M., Neri P., Ratti G., Rappuoli R.;
RT "Cloning and sequencing of the pertussis toxin genes: operon
RT structure and gene duplication";
RL Proc. Natl. Acad. Sci. U.S.A. 83:4631-4635(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=10536;
RX MEDLINE=90045957; PubMed=2554254;
RA Loomore S.M., Cunningham J.D., Bradley W.R., Yao E.L., Dekaban G.A.,
RA Klein M.H.;
RT "A unique sequence of the Bordetella pertussis toxin operon.";
RL Nucleic Acids Res. 17:8365-8365(1989).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=86208173; PubMed=3704651;
RA Loch C., Keith J.M.;
RT "Pertussis toxin gene: nucleotide sequence and genetic organization.";
RL Science 232:1258-1264(1986).

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[4] ACTIVE SITE, AND SEQUENCE OF 153-169.
 MEDLINE=89290006; PubMed=2737291;
 Cockle S.A.;
 "Identification of an active-site residue in subunit S1 of pertussis toxin by photocrosslinking to NAD.";
 FEBS Lett. 249:329-332(1989).
 [5]
 ROLE OF TRYPTOPHAN 60.
 MEDLINE=90008894; PubMed=2551899;
 Cortina G., Barbieri J.T.;
 "Role of tryptophan 26 in the NAD glycohydrolase reaction of the S-1 subunit of pertussis toxin.";
 J. Biol. Chem. 264:17322-17328(1989).
 [6]
 CHARACTERIZATION.
 MEDLINE=91147200; PubMed=1397420;
 Pizzia M., Bugnoli M., Puccini P., Siciliano R., Marino G.,
 Rappuoli R.;
 "Further analysis of the sequence of the S1 subunit of pertussis toxin.";
 Infect. Immun. 59:1177-1179(1991).
 [7]
 ACTIVE SITE, AND CATALYTIC MECHANISM.
 MEDLINE=96051174; PubMed=8527486;
 Loch C., Antoine R.;
 "A proposed mechanism of ADP-ribosylation catalyzed by the pertussis toxin S1 subunit.";
 Biochimie 77:333-340(1995).
 [8]
 X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 STRAIN-10536;
 MEDLINE=94356444; PubMed=8075982;
 Stein P.E., Boodhoo A., Armstrong G.D., Cockle S.A., Klein M.H.,
 Read R.J.;
 "The crystal structure of pertussis toxin.";
 Structure 2:45-57(1994).
 [9]
 X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
 MEDLINE=96219180; PubMed=8637000;
 Hazes B., Boodhoo A., Cockle S.A., Read R.J.;
 "Crystal structure of the pertussis toxin-ATP complex: a molecular sensor.";
 J. Mol. Biol. 258:661-671(1996).
 CC -1- FUNCTION: S1 IS AN NAL-DEPENDENT ADP-RIBOSYLTRANSFERASE. IT CATALYZES THE ADP-RIBOSYLATION OF A CYSTEINE IN THE ALPHA SUBUNIT OF HETEROTRIMERIC G PROTEINS. IN THE ABSENCE OF G PROTEINS IT ALSO CATALYZES THE CLEAVAGE OF NAD(+) INTO ADP-RIBOSE AND NICOTINAMIDE. IT IRREVERSIBLY UNCOUPLES THE G-ALPHA GTP-BINDING PROTEINS FROM THEIR MEMBRANE RECEPTORS.
 CC -1- SUBUNIT: PERTUSSIS TOXIN CONTAINS FIVE DIFFERENT CHAINS, S1-S5. THEY ARE ORGANIZED INTO 2 FUNCTIONAL SUBUNITS: A, COMPOSED OF S1 (WHICH IS TOXIC) AND E, CONTAINING S2, S3, S5, AND TWO COPIES OF S4 (B BINDS TO THE MEMBRANE RECEPTORS). DIMERS OF S2-S4 AND S3-S4 ARE HELD TOGETHER BY S5.
 CC
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 CC
 CC EMBL: M14378; AAA83980.1; -
 CC EMBL: X16347; CAA34397.1; -
 CC EMBL: M13223; AAA22981.1; -
 CC EMBL: A13359; CAA01091.1; -
 CC PIR: A24144; WEBRIP.
 CC PIR: A24394; WEBR11.
 CC PIR: S06588; S06588.
 CC PDB: 1PRT; 26-JAN-95.
 CC PDB: 1BCP; 05-JUN-97.

DR PDB: 1PTO; 15-SEP-95.
 DR InterPro: IPR003898; Borbert-toxa.
 DR Pfam: PF02917; Pertussis_S1; 1.
 DR PRINTS: PR01395; BORPETOXINA.
 KW Toxin; Signal; Transferase; Glycosyltransferase; NAD; Whooping cough;
 KW 3D-structure.
 FT SIGNAL 1 34 PERTUSSIS TOXIN SUBUNIT 1.
 FT CHAIN 35 269 INTERACT WITH NAD.
 FT ACT_SITE 60 60 INCREASE THE NUCLEOPHILICITY OF THE
 FT ACT_SITE 69 69 CYSTEINE IN THE G PROTEIN OR THE WATER
 FT MOLECULE TO ATTACK THE WEAKENED N-
 FT GLYCOSIDIC BOND OF NAD(+) AND YIELD THE
 FT PRODUCTS OF THE REACTION.
 FT EXERTS ITS ACTION ON THE 2'-OH GROUP OF
 FT THE NAD(+), THEREBY FACILITATING
 FT THE FORMATION OF AN OXOCARBONIUM-LIKE
 FT INTERMEDIATE AND THE WEAKENING OF THE N-
 FT GLYCOSIDIC BOND.
 FT DISULFID 75 235 D -> E (IN STRAIN 10536).
 FT VARIANT 68 68 I -> V (IN STRAIN 10536).
 FT VARIANT 232 232 RMAPVIG -> HGAGDS (IN REF. 3).
 FT CONFLICT 227 233
 FT SEQUENCE 269 AA; 29974 MM; F6C88C16DA6B08AB CRC64;
 SQ
 Query Match 7.1%; Score 93; DB 1; Length 269;
 Best Local Similarity 24.0%; Pred. No. 0.23;
 Matches 53; Conservative 22; Mismatches 62; Indels 84; Gaps 11;
 QY 5 LYRADSRPPDEIKRSGGLMPRGHNEYFDRCGTOMNINLYDHARGTGTGFGVRYDDGYVSTSL 64
 Db 41 VRYDSRPPDEVFQN-GFTAGNND-----NVLDTGRSCQGVSSNAFVSTSS 89
 QY 65 SLR-----SAHLAQSLSGSYTYIYIATAPNFWNDVLGVSPHPE 110
 Db 90 SRYTEVYLEHRMQEAVEAERGRG--TGFIYIYEV-RADNNF----- 131
 QY 111 QEVSALGGIPYSOIYGYRVNFGVIDERLHRNREYRDYRVNRLN--IAPAEQGYRLAGFP 168
 Db 132 -----YGAASSYF-----EYVDTYGDNAGRILAGA-----LATYQ 161
 QY 169 PDQAWREPEWIIHAFQGCNSSRT-----ITGDTCEETON 205
 Db 162 SEYLAHRRIP-----PENIRRVTRVYHNGITGETTTEYSN 197
 RESULT 7
 CD36_RAT
 ID CD36_RAT STANDARD; PRT; 471 AA.
 AC Q07969;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Platelet glycoprotein IV (GPIIb) (CD36 antigen) (PAS IV) (PAS-4 protein) (Fatty acid transport protein) (Fatty acid translocase) (Adipocyte membrane protein).
 DE CD36 OR FAT.
 GN Rattus norvegicus (Rat).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Adipocyte;
 RX MEDLINE=93352566; PubMed=7688729;
 RA Abumrad N.A., El-Maghrabi M.R., Amri E.2., Lopez E., Grimaldi P.A.;
 RT "Cloning of a rat adipocyte membrane protein implicated in binding or transport of long-chain fatty acids that is induced during preadipocyte differentiation. Homology with human CD36.";
 RL J. Biol. Chem. 268:17665-17668(1993).
 RN [2]
 RP SEQUENCE FROM N.A.

[illegible]

Db 264 VRFEDGVVISKTYIIRQ-----GEOSLDGFRAWHQVEYRYI-----RFPDGHVWMLTTP 314
QY 107 HPEYQEVSA-----GGIPYQIYGWYRW-----FGVIDERL-HRNREYDRYRNL 153
Db 315 EEPQSTIVPLRTNRTNRTDAILLGHYLSQDTONQTVFAVITKKKEKPLDYKYRFRV 374
QY 154 NIAPAEQYR--LAGFPDQAWREEPWIHHAPOGCGNSRTITGDT 198
Db 375 PVOEADQSFHVLQQLSCSGHORFNKLWIHHS-----CHITYKS-TGET 417

RESULT 10
DHE3_AERPE
ID DHE3_AERPE STANDARD; PRT; 423 AA.
AC Q9YC65;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glutamate dehydrogenase (EC 1.4.1.3) (GDH).
GN GDHA OR APL1386.
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;
OC Aeropyrum.
OX NCBI_TaxID=56636;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RX MEDLINE=99310339; PubMed=10382966;
RA Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
RA Hosoynana A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RT "Complete genome sequence of an aerobic hyper-thermophilic
crenarchaeon, Aeropyrum pernix K1.";
RL DNA Res. 6:83-101(1999).
CC -L-CATALYTIC ACTIVITY: L-glutamate + H(2)O + NAD(P)(+) = 2-oxoglutarate + NH(3) + NAD(P)H.
CC -L SUBUNIT: HOMOHXAMER (BY SIMILARITY).

CC -L SIMILARITY: BELONGS TO THE GLU/LEU/PHE/VAL DEHYDROGENASES FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AP000061; BNA80383.1; -
CC HSP; P96110; I826.
CC InterPro; IPR002086; Aldehyde_dehydr.
CC InterPro; IPR001625; GLFV_dehydrog.
CC InterPro; IPR00205; NAD_binding.
CC Pfam; PF00208; GLFV_dehydrog; 1.
CC Pfam; PF02812; GLFV_dehydrog_N; 1.
CC PRINTS; PR00082; GLFDHNRGNASE.
CC PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.
KW Oxidoreductase; NAD; NADP; Complete proteome.
FT ACT_SITE 110 110 BY SIMILARITY.
FT NP_BIND 222 228 NAD (POTENTIAL).
SQ SEQUENCE 423 AA; 46697 MW; A4B0EA107A89DA62 CRC64;

Query Match 6.6%; Score 86; DB 1; Length 423;
Best Local Similarity 21.9%; Pred. No. 1.8;
Matches 41; Conservative 32; Mismatches 58; Indels 56; Gaps 10;

QY 11 RPPDETKRSGGLMPR-----GHNEYF-----DRGTQMNNINYDHARGTQTFGVRYDDG 58
Db 7 OPTDPLEEARAQLRRVADLLGYDDYVEVLNPRVLRVLT-----IKMDG 54

QY 59 YVSTSLSLRSAHLGOSILSGYSTYYIYVIATAPNMFNVNDVLGVSPHPYEQEVSALGG 118
Db 55 TVTFLGRLSQHSALGPGYKGVRYH-----PNV-TMNEVIALSMMTWK-----NSLAG 103
QY 119 IPYSQIYQWYRVNFGVIDER---LHRNREYDRYRNLN-----IAPAEQYRLAGF 167
Db 104 LPYGGGKGQVYRNPVKILSPRELELSR-----KYFESIDIVGVQDQIPAPVYT----- 153
QY 168 PPDHQAW 174
Db 154 DPQVMSW 160

RESULT 11
CRAA_BACUH
ID CRAA_BACUH STANDARD; PRT; 826 AA.
AC Q9S597;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticidal crystal protein cry27Aa (insecticidal delta-endotoxin
DE CryXXVIIIA(a)) (Crystalline entomocidal protoxin) (94 kDa crystal
DE protein).
GN CRY27AA OR CRYXXVIIIA(A).
OS Bacillus thuringiensis (subsp. higo).
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=132266;
RN [1]
RP SEQUENCE FROM N.A.
RT Saitoh H.;
RT "94kDa mosquitocidal toxin from serovar higo.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
CC -L FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF INSECTS.
CC -L DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -L MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -L SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AB023293; BAA82796.1; -
CC InterPro; IPR001178; Endotoxin.
CC Pfam; PF00555; endotoxin; 1.
KW Toxin; Sporulation.
SQ SEQUENCE 826 AA; 94434 MW; DFD5313C5B6023E2 CRC64;

Query Match 6.5%; Score 84.5; DB 1; Length 826;
Best Local Similarity 21.3%; Pred. No. 5.9;
Matches 44; Conservative 39; Mismatches 83; Indels 41; Gaps 10;

QY 42 YDHARGTQTFGVRYDDGVVSTSLSLSAHLGOSILSGYSTYYIYVIATAPNMFNVN-DV 100
Db 626 YFRARHEHFYIEFD-----TTFSLRNSGQLEHLL-----HIY-----PNTTKISGDQ 670
QY 101 LGVSPHPYEQEVSALGGIPYSQI---YGVYRVNFGVIDERLHRNREYDRYRNLNIAIP 157
Db 671 LLIIDKTEFPV-----GIFLQNTSEGYNTYDQNTSYNQNNYNNQNMDDTYQ-----P 720
QY 158 AEDGYRLAGFPDQAWREEPWIHHAPOGCGNSRSTITGDTFCNEETONLSIYIUREYOS- 216
Db 721 NYDNYK-----QNSSGMYDNPY-NONPKDSYNQNTYDTSYNSQNGVSGNYSNQYNTY 774

```

QY 217 -----KVKQIFSDYQSEVDIYNRIRD 238
Db 775 NQDTENMINOSYNNYNSDNNNNYNSD 801

RESULT 12
PRIO_CRIGR STANDARD; PRT; 254 AA.
AC Q60506;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Major prion protein precursor (PrP) (PrP27-30) (PrP33-35C).
GN PRNP.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=90158578; PubMed=2406562;
RA Lowenstein D.H., Butler D.A., Westaway D., McKinley M.P.,
RA DeArmond S.J., Prusiner S.B.;
RT "Three hamster species with different scrapie incubation times and
RT neuropathological features encode distinct prion proteins.";
RL Mol. Cell. Biol. 10:1153-1163(1990).
CC -!- FUNCTION: THE FUNCTION OF PRP IS NOT KNOWN. PRP IS ENCODED IN THE
CC HOST GENOME AND IS EXPRESSED BOTH IN NORMAL AND INFECTED CELLS.
CC -!- SUBUNIT: PRP HAS A TENDENCY TO AGGREGATE YIELDING POLYMERS CALLED
CC "RODS".
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -!- DISEASE: FOUND IN HIGH QUANTITY IN THE BRAIN OF HUMANS AND ANIMALS
CC INFECTED WITH DEGENERATIVE NEUROLOGICAL DISEASES SUCH AS KURU,
CC CREUTZFELDT-JAKOB DISEASE (CJD), GERSTMANN-STRAUSSLER SYNDROME
CC (GSS), SCRAPIE, BOVINE SPONGIFORM ENCEPHALOPATHY (BSE),
CC TRANSMISSIBLE MINK ENCEPHALOPATHY (TME), ETC.
CC -!- SIMILARITY: BELONGS TO THE PRION FAMILY.
CC
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CC
CC EMBL; M33958; AAA37013.1; -
CC HSSP; P04925; IAG2.
CC InterPro; IPR000817; Prion.
CC Pfam; PF00377; prion; 1.
CC PRINTS; PR00341; PRION.
CC SMART; SM00157; PRP; 1.
CC PROSITE; PS00291; PRION_1; 1.
CC PROSITE; PS00706; PRION_2; 1.
CC SIGNAL 1 22
CC Chain 23 231
CC MAJOR PRION PROTEIN.
CC REMOVED IN MATURE FORM.
CC PROPEP 232 254
CC LIPID 231 231
CC DOMAIN 90 231
CC CARBOHYD 181 181
CC CARBOHYD 197 197
CC DISULFID 179 214
CC DOMAIN 51 91
CC Q.
CC REPEAT 51 59
CC REPEAT 60 67
CC REPEAT 68 75
CC REPEAT 76 83
CC REPEAT 84 91
CC SEQUENCE 254 AA; 27823 MW; 6299CA000EB8607D CRC64;

Query Match 6.4%; Score 83; DB 1; Length 254;
Best Local Similarity 25.0%; Pred. No. 1.8;
Matches 31; Conservative 20; Mismatches 51; Indels 22; Gaps 6;

QY 114 SALGGIPYSQIYGYRVNFGVIDERLHNRNRYRDRYR-NNIAPAEQGYRLAGFPDPHQ 172
Db 120 AVVGGL-----GGYMLGSAMSRPMLHFGNDWEDRYRNNRYPNQVYR-----PVDQ 168
QY 173 AWREEPWIHHAPOCGGN---SSRTIGTDCNEETQNLSTIYLREYQSKVKQIFSDYQSE 229
Db 169 YNNQNNVH-----DCVNITIKQHTVTTTKE---NFTETDKMVERVVEQMCVTQYQKE 221
QY 230 VDIY 233
Db 222 SQAY 225

RESULT 13
PRIO_CRIMI STANDARD; PRT; 254 AA.
AC Q60468;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Major prion protein precursor (PrP) (PrP27-30) (PrP33-35C).
GN PRNP.
OS Cricetus migratorius (Armenian hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetus.
OX NCBI_TaxID=10032;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=90158578; PubMed=2406562;
RA Lowenstein D.H., Butler D.A., Westaway D., McKinley M.P.,
RA DeArmond S.J., Prusiner S.B.;
RT "Three hamster species with different scrapie incubation times and
RT neuropathological features encode distinct prion proteins.";
RL Mol. Cell. Biol. 10:1153-1163(1990).
CC -!- FUNCTION: THE FUNCTION OF PRP IS NOT KNOWN. PRP IS ENCODED IN THE
CC HOST GENOME AND IS EXPRESSED BOTH IN NORMAL AND INFECTED CELLS.
CC -!- SUBUNIT: PRP HAS A TENDENCY TO AGGREGATE YIELDING POLYMERS CALLED
CC "RODS".
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -!- DISEASE: FOUND IN HIGH QUANTITY IN THE BRAIN OF HUMANS AND ANIMALS
CC INFECTED WITH DEGENERATIVE NEUROLOGICAL DISEASES SUCH AS KURU,
CC CREUTZFELDT-JAKOB DISEASE (CJD), GERSTMANN-STRAUSSLER SYNDROME
CC (GSS), SCRAPIE, BOVINE SPONGIFORM ENCEPHALOPATHY (BSE),
CC TRANSMISSIBLE MINK ENCEPHALOPATHY (TME), ETC.
CC -!- SIMILARITY: BELONGS TO THE PRION FAMILY.
CC
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CC
CC EMBL; M33959; AAA37014.1; -
CC HSSP; P04925; IAG2.
CC InterPro; IPR000817; Prion.
CC Pfam; PF00377; prion; 1.
CC PRINTS; PR00341; PRION.
CC SMART; SM00157; PRP; 1.
CC PROSITE; PS00291; PRION_1; 1.
CC PROSITE; PS00706; PRION_2; 1.
CC SIGNAL 1 22
CC Chain 23 231
CC MAJOR PRION PROTEIN.

```


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OM protein - protein search, using sw model

Run on: June 10, 2002, 17:30:53 ; Search time 26.47 seconds
(without alignments)
1568.522 Million cell updates/sec

Title: US-09-297-171-1
Perfect score: 1304
Sequence: 1 NGRDLRYRADSRPPDEIKRSG.....QIFSDYQSEVDIYNRDEL 240

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacterioplasmid:*
17: sp_archaeplastid:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1290	98.9	258	2	066280
2	357	27.4	68	2	047182
3	152	11.7	46	2	057372
4	94	7.2	850	5	09U8Q4
5	93	7.1	269	2	069258
6	93	7.1	850	5	09GV36
7	91	7.0	392	10	081497
8	90.5	6.9	702	5	024995
9	89	6.8	269	2	093V22
10	88.5	6.8	332	3	002796
11	88	6.7	269	2	070057
12	88	6.7	547	4	09NT57
13	87	6.7	809	3	094527
14	86.5	6.6	145	16	09JZ10
15	85.5	6.6	256	6	095N12
16	85.5	6.6	435	17	09YB04

17	84	6.4	1219	12	09IMU3
18	83.5	6.4	524	5	09VLE2
19	83.5	6.4	715	5	0961P3
20	83.5	6.4	870	2	003988
21	83	6.4	353	16	097N09
22	83	6.4	7829	5	018559
23	82.5	6.3	888	3	09UVU7
24	82	6.3	215	6	097904
25	82	6.3	216	6	09TV00
26	82	6.3	235	6	097695
27	82	6.3	446	5	09WOC6
28	82	6.3	556	3	096UL8
29	81.5	6.2	419	11	070572
30	81.5	6.2	594	8	09T3A0
31	81.5	6.2	753	5	025050
32	81	6.2	200	6	097912
33	81	6.2	204	2	09LIE4
34	81	6.2	899	2	09R2J7
35	81	6.2	899	2	052336
36	81	6.2	968	10	09LUL8
37	80.5	6.2	173	12	092395
38	80.5	6.2	533	2	09A054
39	80.5	6.2	547	12	0911K0
40	80.5	6.2	549	12	09DX74
41	80.5	6.2	570	10	065813
42	80.5	6.2	888	3	09C209
43	80	6.1	212	6	097698
44	80	6.1	243	11	097895
45	80	6.1	256	6	062670

ALIGNMENTS

RESULT 1

066280 ID 066280 PRELIMINARY; PRT; 258 AA.
AC 066280; 1998 (TREMREL. 07, Created)
DT 01-AUG-1998 (TREMREL. 07, Last sequence update)
DT 01-JUN-2001 (TREMREL. 17, Last annotation update)
DE HEAT-LABILE ENTEROTOXIN A SUBUNIT.
GN LTH A SUBUNIT.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-1032 (ENTEROTOXIGENIC);
RA Komase K.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN-1032 (ENTEROTOXIGENIC);
RX MEDLINE=9501056; PubMed=7998417;
RA Tamura S., Asanuma H., Tomita T., Komase K., Kawahara K., Danbara H.,
Hattori N., Watanabe K., Suzuki Y., Nagamine T., Aizawa C., Oya A.,
Kurata T.;
RT "Escherichia coli heat-labile enterotoxin B subunits supplemented with
a trace amount of the holotoxin as an adjuvant for nasal influenza
vaccine".
RL Vaccine 12:1083-1089(1994).
DR EMBL; AB011677; BAA25725.1; -.
DR HSP; P06717; LTG.
DR InterPro; IPR001144; Enterotoxin_A.
DR InterPro; IPR000886; ER target.
DR Pfam; PF01375; Enterotoxin_A; 1.
DR PRINTS; PRQ0771; ENTEROTOXIN.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
SQ SEQUENCE 258 AA; 29931 MW; 2BB15D27740EB788 CRC64;

Query Match 98.9%; Score 1290; DB 2; Length 258;
Best Local Similarity 98.8%; Pred. No. 1.4e-110;
Matches 237; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NGDRLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTOMNINLYDHARGTQTGTFVRYDDGYV 60
DB 19 NGDKLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTOMNINLYDHARGTQTGTFVRYDDGYV 78
QY 61 STSLSLRAHLAAGSILSGYSTYIYVIATAPNMFNVNDLVGYSPHPYEGEVSALGGIP 120
DB 79 STSLSLRAHLAAGSILSGYSTYIYVIATAPNMFNVNDLVGYSPHPYEGEVSALGGIP 138
QY 121 YSQIYGYRVNFGVIDERLHNRREYDRYRNLNIAPAEDGYRLAGPPPDHQAWAREPWI 180
DB 139 YSQIYGYRVNFGVIDERLHNRREYDRYRNLNIAPAEDGYRLAGPPPDHQAWAREPWI 198
QY 181 HHAPOGCGNSRRTITGTCNEETQNLSTIYLRYQSKVKRQIFSDYQSEVDIYNRIDEL 240
DB 199 HHAPOGCGNSRRTITGTCNEETQNLSTIYLRYQSKVKRQIFSDYQSEVDIYNRIDEL 258

RESULT 2
Q47182 PRELIMINARY; PRT; 68 AA.
AC Q47182
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ENTEROTOXIN A (FRAGMENT).
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE OF 64-68 FROM N.A.
RC STRAIN=H10407;
RX MEDLINE=83007048; PubMed=6749816;
RA Yamamoto T., Tamura T., Ryoji M., Kaji A., Yokota T., Takano T.;
RT "Sequence analysis of the heat-labile enterotoxin subunit B gene
originating in human enterotoxigenic Escherichia coli.";
RL J. Bacteriol. 152:506-509(1982).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=H10407;
RX MEDLINE=83114628; PubMed=6759877;
RA Yamamoto T., Tamura T., Yokota T., Takano T.;
RT "Overlapping genes in the heat-labile enterotoxin operon originating
from Escherichia coli human strain.";
RL Mol. Gen. Genet. 188:356-359(1982).
RN [3]
RP -SEQUENCE OF 64-68 FROM N.A.
RC STRAIN=H10407;
RX MEDLINE=83265593; PubMed=6348025;
RA Yamamoto T., Yokota T.;
RT "Sequence of heat-labile enterotoxin of Escherichia coli pathogenic
for humans";
RL J. Bacteriol. 155:728-733(1983).
DR EMBL; J01646; AAB02981.1; -;
DR HSSP; P06717; 1LT3.
DR InterPro; IPR001144; Enterotoxin_A.
DR InterPro; IPR000886; ER_target.
DR Pfam; PF01375; Enterotoxin_A.1.
DR PRINTS; PR00771; ENTEROTOXINA.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 68 AA; 8077 MW; 673CDB4D2E884854 CRC64;

Query Match 27.4%; Score 357; DB 2; Length 68;
Best Local Similarity 95.6%; Pred. No. 1.2e-25;
Matches 65; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 173 AWREEPWIHAPOGCGNSRRTITGTCNEETQNLSTIYLRYQSKVKRQIFSDYQSEVDI 232

Db 1 AWREEPWIHAPOGCGNSRRTITGTCNEETQNLSTIYLRYQSKVKRQIFSDYQSEVDI 60
QY 233 YNRIDEL 240
DB 61 YNRIDEL 68
RESULT 3
Q57372 PRELIMINARY; PRT; 46 AA.
AC Q57372
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CHOLERA TOXIN A2.
GN CTA2.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=42608;
RX MEDLINE=94237453; PubMed=8181723;
RA Lebens M., Holmgren J.;
RT "Structure and arrangement of the cholera toxin genes in Vibrio
cholerae O139.";
RL FEMS Microbiol. Lett. 117:197-202(1994).
DR EMBL; X76391; CAA53975.1; -;
DR EMBL; X76390; CAA53974.1; -;
DR HSSP; P01555; 1XTC.
DR InterPro; IPR001144; Enterotoxin_A.
DR InterPro; IPR000886; ER_target.
DR Pfam; PF01375; Enterotoxin_A.1.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
SQ SEQUENCE 46 AA; 5447 MW; 1B6085A02E8889D6 CRC64;

Query Match 11.7%; Score 152; DB 2; Length 46;
Best Local Similarity 63.6%; Pred. No. 4.8e-07;
Matches 28; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 197 DTCNEETQNLSTIYLRYQSKVKRQIFSDYQSEVDIYNRIDEL 240
DB 3 NTCDERTQSLGKFLDEYQSKVKRQYFGYQSDIDTHNRINDEL 46
RESULT 4
Q90804 PRELIMINARY; PRT; 850 AA.
AC Q90804
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PIERISIN.
OS Pteris rapae.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Papilionoidea; Pieridae; Pierinae; Pieris.
OX NCBI_TaxID=64459;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99415906; PubMed=10485873;
RA Watanabe M., Kono T., Matsushima-Hibiya Y., Kanazawa T., Nishisaka N.,
RA Kishimoto T., Koyama K., Sugimura T., Wakabayashi K.;
RT "Molecular cloning of an apoptosis-inducing protein, pierisin, from
cabbage butterfly: Possible involvement of ADP-ribosylation in its
activity.";
RT activity.";
RL Procl. Natl. Acad. Sci. U.S.A. 96:10608-10613(1999).
DR EMBL; AB030305; BAA84491.1; -;
DR InterPro; IPR000772; Ricin_B_lectin.
DR Pfam; PF00652; Ricin_B_lectin; 8.
DR SMART; SM00458; RICIN; 4.

INTERFERENCE

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 10, 2002, 17:15:38 ; Search time 12.93 Seconds
(without alignments)
453.375 Million cell updates/sec

Title: US-09-297-171-1
Perfect score: 1304
Sequence: 1 NGDRLRADSRPPDEIKRSG.....QIFSDYQSEVDIYNIRDEL 240

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/2/iaa/5A.COMB.pcp.*
- 2: /cgn2_6/ptodata/2/iaa/5B.COMB.pcp.*
- 3: /cgn2_6/ptodata/2/iaa/6A.COMB.pcp.*
- 4: /cgn2_6/ptodata/2/iaa/6B.COMB.pcp.*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS.COMB.pcp.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pcp.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1299	99.6	240	4	US-08-823-120-3
2	1183	90.7	236	4	US-08-823-120-6
3	1183	90.7	254	3	US-08-486-099-114
4	1183	90.7	254	3	US-08-360-107A-124
5	1183	90.7	254	3	US-08-484-223B-114
6	1183	90.7	254	3	US-08-919-597-114
7	1183	90.7	254	3	US-08-475-668A-114
8	1183	90.7	254	3	US-08-485-551A-114
9	1183	90.7	254	3	US-08-471-913A-114
10	1183	90.7	254	4	US-08-485-264A-114
11	1183	90.7	254	4	US-08-474-349A-114
12	1088	83.4	240	2	US-08-435-605A-13
13	1088	83.4	240	4	US-08-823-120-4
14	1088	83.4	240	4	US-08-823-120-8
15	1088	83.4	258	1	US-08-449-045C-2
16	1088	83.4	258	2	US-08-435-605A-2
17	1088	83.4	258	6	5223610-2
18	1085	83.2	240	2	US-08-435-605A-15
19	1085	83.2	240	2	US-08-435-605A-51
20	1085	83.2	240	2	US-08-435-605A-56
21	1084	83.1	240	2	US-08-435-605A-52
22	1084	83.1	240	2	US-08-435-605A-53
23	1081	82.9	240	2	US-08-435-605A-49
24	1081	82.9	240	2	US-08-435-605A-50
25	972	74.5	238	4	US-08-823-120-2
26	940	72.1	194	2	US-08-435-605A-54
27	934	71.6	194	2	US-08-435-605A-6

28	934	71.6	194	2	US-08-435-605A-14	Sequence 14, Appl
29	933	71.5	192	2	US-08-435-605A-8	Sequence 8, Appl
30	931	71.4	194	2	US-08-435-605A-16	Sequence 16, Appl
31	925	70.9	194	2	US-08-435-605A-55	Sequence 55, Appl
32	871	66.8	179	2	US-08-435-605A-57	Sequence 57, Appl
33	638.5	49.0	241	4	US-08-823-120-1	Sequence 1, Appl
34	157	12.0	46	2	US-08-435-605A-10	Sequence 10, Appl
35	103	7.9	20	1	US-08-171-299B-11	Sequence 11, Appl
36	96	7.4	20	1	US-08-171-299B-10	Sequence 10, Appl
37	93	7.1	266	6	5223610-5	Patent No. 5223610
38	89	6.8	269	6	5433945-5	Patent No. 5433945
39	88	6.7	1584	4	US-09-251-645-6	Sequence 6, Appl
40	86	6.6	15	3	US-08-296-848A-2	Sequence 2, Appl
41	83.5	6.4	687	1	US-08-204-656B-10	Sequence 10, Appl
42	82.5	6.3	417	4	US-08-462-467B-6	Sequence 6, Appl
43	82.5	6.3	417	4	US-08-462-467B-10	Sequence 10, Appl
44	82.5	6.3	556	4	US-08-462-467B-24	Sequence 24, Appl
45	82.5	6.3	556	4	US-08-462-467B-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-08-823-120-3
; Sequence 3, Application US/08823120
; Patent No. 6149919
; GENERAL INFORMATION:
; APPLICANT: Domenighini, Mario
; APPLICANT: Rappuoli, Rino
; APPLICANT: Pizza, Mariagrazia
; TITLE OF INVENTION: Immunogenic Detoxified Mutants of
; TITLE OF INVENTION: Cholera Toxin and of the Toxin Lt, Their Preparation and
; TITLE OF INVENTION: Their Use for the Preparation of Vaccines
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: California
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/823,120
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/256,003
; FILING DATE: 11-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: McClung, Barbara G.
; REGISTRATION NUMBER: 33,113
; REFERENCE/DOCKET NUMBER: 0315.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2708
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-823-120-3.

Query Match 99.6%; Score 1299; DB 4; Length 240;
Best Local Similarity 99.6%; Pred. No. 1.1e-142;

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Matches 239; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 NGDRLYRADSRPPDEIKRSGLMPRGHNEYFDRGTQNMNINLYDHARGTQTGFVRYDDGYV 60
Db 1 NGDRLYRADSRPPDEIKRSGLMPRGHNEYFDRGTQNMNINLYDHARGTQTGFVRYDDGYV 60
Qy 61 STSLSLSAHLAAGSILSGYSTYYIYVIATAPNMFNNDVLGVYSPHPYEQEVSALGGIP 120
Db 61 STSLSLSAHLAAGSILSGYSTYYIYVIATAPNMFNNDVLGVYSPHPYEQEVSALGGIP 120
Qy 121 YSQIYGWYRVNFGVIDERLHNRNREYRDYRNLNIAPAEDGYRLAGPPDHOAWREPEWI 180
Db 121 YSQIYGWYRVNFGVIDERLHNRNREYRDYRNLNIAPAEDGYRLAGPPDHOAWREPEWI 180
Qy 181 HPAQGGCGNSRRTTGTCTCNEETQNLSTIYLREYQSKVKRQIFSDYOSEVDIYNRIRDEL 240
Db 181 HPAQGGCGNSRRTTGTCTCNEETQNLSTIYLREYQSKVKRQIFSDYOSEVDIYNRIRDEL 240
RESULT 2
US-08-823-120-6
; Sequence 6, Application US/08823120
; Patent No. 6149919
; GENERAL INFORMATION:
; APPLICANT: Domenighini, Mario
; APPLICANT: Rappuoli, Rino
; APPLICANT: Pizza, Mariagrazia
; TITLE OF INVENTION: Immunogenic Detoxified Mutants of
; TITLE OF INVENTION: Cholera Toxin and of the Toxin Lt, Their Preparation and
; TITLE OF INVENTION: Their Use for the Preparation of Vaccines
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: California
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/823,120
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/256,003
; FILING DATE: 11-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: McClung, Barbara G.
; REGISTRATION NUMBER: 33,113
; REFERENCE/DOCKET NUMBER: 0315.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2708
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-823-120-6
Query Match 90.7%; Score 1183; DB 4; Length 236;
Best Local Similarity 93.3%; Pred. No. 3.2e-129;
Matches 224; Conservative 2; Mismatches 10; Indels 4; Gaps 2;
Qy 1 NGDRLYRADSRPPDEIKRSGLMPRGHNEYFDRGTQNMNINLYDHARGTQTGFVRYDDGYV 60
Db 1 NGDRLYRADSRPPDEIKRSGLMPRG-NEYFDRGTQNMNINLYDHARGTQTGFVRYDDGYV 59
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Qy 61 STSLSLSAHLAAGSILSGYSTYYIYVIATAPNMFNNDVLGVYSPHPYEQEVSALGGIP 120
Db 60 STSLSLSAHLAAGIILSGISLTIYVIA---NMFNNDVIVISVSPHPYEQEVSALGGIP 116
Qy 121 YSQIYGWYRVNFGVIDERLHNRNREYRDYRNLNIAPAEDGYRLAGPPDHOAWREPEWI 180
Db 117 YSQIYGWYRVNFGVIDERLHNRNREYRDYRNLNIAPAEDGYRLAGPPDHOAWREPEWI 176
Qy 181 HPAQGGCGNSRRTTGTCTCNEETQNLSTIYLREYQSKVKRQIFSDYOSEVDIYNRIRDEL 240
Db 177 HPAQGGCGSDSRTTGTCTCNEETQNLSTIYLREYQSKVKRQIFSDYOSEVDIYNRIRDEL 236
RESULT 3
US-08-486-099-114
; Sequence 114, Application US/08486099
; Patent No. 6013263
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
; TITLE OF INVENTION: B VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,099
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-486-099-114
Query Match 90.7%; Score 1183; DB 3; Length 254;
Best Local Similarity 93.3%; Pred. No. 3.6e-129;
Matches 224; Conservative 2; Mismatches 10; Indels 4; Gaps 2;
Qy 1 NGDRLYRADSRPPDEIKRSGLMPRGHNEYFDRGTQNMNINLYDHARGTQTGFVRYDDGYV 60
Db 19 NGDRLYRADSRPPDEIKRFRSLMPRG-NEYFDRGTQNMNINLYDHARGTQTGFVRYDDGYV 77
Qy 61 STSLSLSAHLAAGSILSGYSTYYIYVIATAPNMFNNDVLGVYSPHPYEQEVSALGGIP 120
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Db 78 STSLSRSAHLAGQYILSGYSLTIYIVIA---NMFNVDIVSYSPHPYQEVYSGALGGIP 134
QY 121 YSQIYGWRYNFGVIDERLHNRNREYDRYRNINLAPAEADGYRLAGPPDPHQAWAREEPWI 180
Db 135 YSQIYGWRYNFGVIDERLHNRNREYDRYRNINLAPAEADGYRLAGPPDPHQAWAREEPWI 194
QY 181 HHAPOGGGNSRRTTGTDCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIDEL 240
Db 195 HHAPOGGGDSRRTTGTDCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIDEL 254

RESULT 4
US-08-360-107A-124
; Sequence 124, Application US/08360107A
; Patent No. 6017536
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 149
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,107A
; FILING DATE: 20-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 124:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-360-107A-124

Query Match 90.7%; Score 1183; DB 3; Length 254;
Best Local Similarity 93.3%; Pred. No. 3.6e-129;
Matches 224; Conservative 2; Mismatches 10; Indels 4; Gaps 2;
QY 1 NGDRLYRADSRPDEIKRSGGLMPRGHNEYFDRGTQNNINLYDHARTQTGFVRYDDGYV 60
Db 19 NGDRLYRADSRPDEIKRFSRLMPRG-NEYFDRGTQNNINLYDHARTQTGFVRYDDGYV 77
QY 61 STSLSRSAHLAGQSLSGSYSTIYIVIA---NMFNVDIVSYSPHPYQEVYSGALGGIP 120
Db 78 STSLSRSAHLAGQYILSGYSLTIYIVIA---NMFNVDIVSYSPHPYQEVYSGALGGIP 134

QY 121 YSQIYGWRYNFGVIDERLHNRNREYDRYRNINLAPAEADGYRLAGPPDPHQAWAREEPWI 180
Db 135 YSQIYGWRYNFGVIDERLHNRNREYDRYRNINLAPAEADGYRLAGPPDPHQAWAREEPWI 194
QY 181 HHAPOGGGNSRRTTGTDCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIDEL 240
Db 195 HHAPOGGGDSRRTTGTDCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIDEL 254

RESULT 5
US-08-484-223B-114
; Sequence 114, Application US/08484223B
; Patent No. 6020459
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 245
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-484-223B-114

Query Match 90.7%; Score 1183; DB 3; Length 254;
Best Local Similarity 93.3%; Pred. No. 3.6e-129;
Matches 224; Conservative 2; Mismatches 10; Indels 4; Gaps 2;
QY 1 NGDRLYRADSRPDEIKRSGGLMPRGHNEYFDRGTQNNINLYDHARTQTGFVRYDDGYV 60
Db 19 NGDRLYRADSRPDEIKRFSRLMPRG-NEYFDRGTQNNINLYDHARTQTGFVRYDDGYV 77
QY 61 STSLSRSAHLAGQSLSGSYSTIYIVIA---NMFNVDIVSYSPHPYQEVYSGALGGIP 120
Db 78 STSLSRSAHLAGQYILSGYSLTIYIVIA---NMFNVDIVSYSPHPYQEVYSGALGGIP 134
QY 121 YSQIYGWRYNFGVIDERLHNRNREYDRYRNINLAPAEADGYRLAGPPDPHQAWAREEPWI 180

Db 135 YSOIYGWYRVNFGVIDERLHNRNREYDRYRNLNIAPAEDGYRLAGFPDQAWREBPWI 194
QY 181 HHAPOGCGNSRRTTGTDCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIDEL 240
Db 195 HHAPOGCGDSSRRTTGTDCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIDEL 254

RESULT 6

US-08-919-597-114
; Sequence 114, Application US/08919597
; Patent No. 6054265
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/919,597
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470,896
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-919-597-114

Query Match 90.7%; Score 1183; DB 3; Length 254;
Best Local Similarity 93.3%; Pred. No. 3.6e-129;
Matches 224; Conservative 2; Mismatches 10; Indels 4; Gaps 2;

QY 1 NGRDLRADSRPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTGTGFVYDDGYV 60
Db 19 NGRDLRADSRPDEIKRFSRLMPRG-NEYFDRGTQMNINLYDHARGTGTGFVYDDGYV 77
QY 61 STSLRSRAHLAQOSILSGYSTYIYVIATAPNMFNNDVLGYVSPHPYEOEVSALGGIP 120
Db 78 STSLRSRAHLAQYILSGYSLTIYIVIA---NMFNNDVISYSPHPYEQEVSALGGIP 134

QY 121 YSOIYGWYRVNFGVIDERLHNRNREYDRYRNLNIAPAEDGYRLAGFPDQAWREBPWI 180
Db 135 YSOIYGWYRVNFGVIDERLHNRNREYDRYRNLNIAPAEDGYRLAGFPDQAWREBPWI 194
QY 181 HHAPOGCGNSRRTTGTDCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIDEL 240
Db 195 HHAPOGCGDSSRRTTGTDCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIDEL 254

RESULT 7

US-08-475-668A-114
; Sequence 114, Application US/08475668A
; Patent No. 6060065
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,668A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-475-668A-114

Query Match 90.7%; Score 1183; DB 3; Length 254;
Best Local Similarity 93.3%; Pred. No. 3.6e-129;
Matches 224; Conservative 2; Mismatches 10; Indels 4; Gaps 2;

QY 1 NGRDLRADSRPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTGTGFVYDDGYV 60
Db 19 NGRDLRADSRPDEIKRFSRLMPRG-NEYFDRGTQMNINLYDHARGTGTGFVYDDGYV 77
QY 61 STSLRSRAHLAQOSILSGYSTYIYVIATAPNMFNNDVLGYVSPHPYEOEVSALGGIP 120
Db 78 STSLRSRAHLAQYILSGYSLTIYIVIA---NMFNNDVISYSPHPYEQEVSALGGIP 134
QY 121 YSOIYGWYRVNFGVIDERLHNRNREYDRYRNLNIAPAEDGYRLAGFPDQAWREBPWI 180
Db 135 YSOIYGWYRVNFGVIDERLHNRNREYDRYRNLNIAPAEDGYRLAGFPDQAWREBPWI 194
QY 181 HHAPOGCGNSRRTTGTDCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIDEL 240

Db 195 HHAPOCGDSSRTITGTCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIDEL 254

RESULT 8

US-08-485-551A-114
; Sequence 114, Application US/0848551A
; Patent No. 6068973
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,551A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-023
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-485-551A-114

Query Match 90.7%; Score 1183; DB 3; Length 254;
Best Local Similarity 93.3%; Pred. No. 3.6e-129;
Matches 224; Conservative 2; Mismatches 10; Indels 4; Gaps 2;

QY 1 NGRDLRADSRPPDEIKRSGGLMPRGHNEYFDRGTQNNINLYDHARGTQTGFVRYDDGYV 60
Db 19 NGRDLRADSRPPDEIKRFRSLMPRG-NEYFDRGTQNNINLYDHARGTQTGFVRYDDGYV 77
QY 61 STSLSRSAHLAQOSTLSCYSTIYYIYIATAPNMFNNDVLGVYSPHPYEQEVSALGGIP 120
Db 78 STSLSRSAHLAQYILSGYSLTIIYIVIA---NMFNNDVISVSPHPYEQEVSALGGIP 134
QY 121 YSOIYGWYRVNFGVIDERLHRNREYDRYRNLIAPAEDGYRLAGFPDPHQAWREPWI 180
Db 135 YSOIYGWYRVNFGVIDERLHRNREYDRYRNLIAPAEDGYRLAGFPDPHQAWREPWI 194
QY 181 HHAPOCGDSSRTITGTCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIDEL 240
Db 195 HHAPOCGDSSRTITGTCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIDEL 254

RESULT 10

RESULT 9

US-08-471-913A-114
; Sequence 114, Application US/08471913A
; Patent No. 6093794
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 214
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,913A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-471-913A-114

Query Match 90.7%; Score 1183; DB 3; Length 254;
Best Local Similarity 93.3%; Pred. No. 3.6e-129;
Matches 224; Conservative 2; Mismatches 10; Indels 4; Gaps 2;

QY 1 NGRDLRADSRPPDEIKRSGGLMPRGHNEYFDRGTQNNINLYDHARGTQTGFVRYDDGYV 60
Db 19 NGRDLRADSRPPDEIKRFRSLMPRG-NEYFDRGTQNNINLYDHARGTQTGFVRYDDGYV 77
QY 61 STSLSRSAHLAQOSTLSCYSTIYYIYIATAPNMFNNDVLGVYSPHPYEQEVSALGGIP 120
Db 78 STSLSRSAHLAQYILSGYSLTIIYIVIA---NMFNNDVISVSPHPYEQEVSALGGIP 134
QY 121 YSOIYGWYRVNFGVIDERLHRNREYDRYRNLIAPAEDGYRLAGFPDPHQAWREPWI 180
Db 135 YSOIYGWYRVNFGVIDERLHRNREYDRYRNLIAPAEDGYRLAGFPDPHQAWREPWI 194
QY 181 HHAPOCGDSSRTITGTCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIDEL 240
Db 195 HHAPOCGDSSRTITGTCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIDEL 254

US-08-485-264A-114
; Sequence 114, Application US/08485264A
; Patent No. 6228983
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
; TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,264A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-485-264A-114

Query Match 90.7%; Score 1183; DB 4; Length 254;
Best Local Similarity 93.3%; Pred. No. 3.6e-129;
Matches 224; Conservative 2; Mismatches 10; Indels 4; Gaps 2;
QY 1 NGRDLRADSRPPDEIKRSGGLMPRGHNEYFDRGTOMNINLYDHARGTQTGFVRYDDGYV 60
DB 19 NGRDLRADSRPPDEIKRFRSLMPRG-NEYFDRGTOMNINLYDHARGTQTGFVRYDDGYV 77
QY 61 STSLRSRAHLAQSIILSGSYTYIIYVIATAPNMFNNDVLGYSPHPYEQEVSALCGIP 120
DB 78 STSLRSRAHLAQSIILSGSYTYIIYVIA---NMFNNDVIVSYSPHPYEQEVSALCGIP 134
QY 121 YSOIYGWYRVNFGVDERLHRNREYRDYRNINIAPAEDGYRLAGFPDPHQAWREEPWI 180
DB 135 YSOIYGWYRVNFGVDERLHRNREYRDYRNINIAPAEDGYRLAGFPDPHQAWREEPWI 194
QY 181 HHAPOCGGSSRTTGTCTNEETQNLSTIYLYREYQSKVKRQIFSDYQSEVDIYNRIRDEL 240
DB 195 HHAPOCGGSSRTTGTCTNEETQNLSTIYLYREYQSKVKRQIFSDYQSEVDIYNRIRDEL 254

RESULT 11
US-08-474-349A-114
; Sequence 114, Application US/08474349A

..

Patent No. 6333395
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
; TITLE OF INVENTION: VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 517
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-474-349A-114

Query Match 90.7%; Score 1183; DB 4; Length 254;
Best Local Similarity 93.3%; Pred. No. 3.6e-129;
Matches 224; Conservative 2; Mismatches 10; Indels 4; Gaps 2;
QY 1 NGRDLRADSRPPDEIKRSGGLMPRGHNEYFDRGTOMNINLYDHARGTQTGFVRYDDGYV 60
DB 19 NGRDLRADSRPPDEIKRFRSLMPRG-NEYFDRGTOMNINLYDHARGTQTGFVRYDDGYV 77
QY 61 STSLRSRAHLAQSIILSGSYTYIIYVIATAPNMFNNDVLGYSPHPYEQEVSALCGIP 120
DB 78 STSLRSRAHLAQSIILSGSYTYIIYVIA---NMFNNDVIVSYSPHPYEQEVSALCGIP 134
QY 121 YSOIYGWYRVNFGVDERLHRNREYRDYRNINIAPAEDGYRLAGFPDPHQAWREEPWI 180
DB 135 YSOIYGWYRVNFGVDERLHRNREYRDYRNINIAPAEDGYRLAGFPDPHQAWREEPWI 194
QY 181 HHAPOCGGSSRTTGTCTNEETQNLSTIYLYREYQSKVKRQIFSDYQSEVDIYNRIRDEL 240
DB 195 HHAPOCGGSSRTTGTCTNEETQNLSTIYLYREYQSKVKRQIFSDYQSEVDIYNRIRDEL 254

RESULT 12
US-08-435-605A-13
; Sequence 13, Application US/08435605A
; Patent No. 5874287
; GENERAL INFORMATION:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/823,120
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/256,003
FILING DATE: 11-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: McClung, Barbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0315,001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2708
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 240 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-823-120-8

Query Match 83.4%; Score 1088; DB 4; Length 240;
Best Local Similarity 81.7%; Pred. No. 3.5e-118;
Matches 196; Conservative 24; Mismatches 20; Indels 0; Gaps 0;
QY 1 NGRLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQNNINLYDHARTGTGTFVRYDDGYV 60
Db 1 NDDKLYRADSRPPDEIKRSGGLMPRGQSEYFDRGTQNNINLYDHARTGTGTFVRHDDGYV 60
QY 61 STSLSRSAHLGOSILSGYSTYIYVIATAPNNFNVDVGLVYSPHPYEQEVSALGGIP 120
Db 61 STSLSRSAHLVGQTIILSGHSTYIYVIATAPNNFNVDVGLVYSPHPDEQVSALGGIP 120
QY 121 YSQIYGWYRVNFGVIDERLHNRNRYDRYRNLIAPAEDGYRLAGFPDQAWREEPWI 180
Db 121 YSQIYGWYRVHFGVLDQLHNRNGYDRYYSNLDIAPAADGYGLAGFPPEHRAWREEPWI 180
QY 181 HHAPQCGNSRRTITGTCNEETQNLSTIYLYREYQSKVKRQIFSDYQSEVDIYNRIDEL 240
Db 181 HHAPPGCGNAPRSSISNTCDKFTQSLGKFLDEYQSKVKRQIFSGYQSDIDTHNRKDEL 240

RESULT 15
US-08-449-045C-2
Sequence 2, Application US/08449045C
Patent No. 5770203
GENERAL INFORMATION:
APPLICANT: Burnette, Neal W.
APPLICANT: Kaslow, Harvey R.
TITLE OF INVENTION: RECOMBINANT DNA-DERIVED CHOLERA TOXIN
TITLE OF INVENTION: SUBUNIT ANALOGS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 De Havilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,045C
FILING DATE: 24-MAY-1995
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/694,733
FILING DATE: 02-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/271,222
FILING DATE: 06-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mazza, Richard J.
REGISTRATION NUMBER: 27,657
REFERENCE/DOCKET NUMBER: A-196C
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 258 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-449-045C-2
Query Match 83.4%; Score 1088; DB 1; Length 258;
Best Local Similarity 81.7%; Pred. No. 3.9e-118;
Matches 196; Conservative 24; Mismatches 20; Indels 0; Gaps 0;
QY 1 NGRLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQNNINLYDHARTGTGTFVRYDDGYV 60
Db 19 NDDKLYRADSRPPDEIKRSGGLMPRGQSEYFDRGTQNNINLYDHARTGTGTFVRHDDGYV 78
QY 61 STSLSRSAHLGOSILSGYSTYIYVIATAPNNFNVDVGLVYSPHPYEQEVSALGGIP 120
Db 79 STSLSRSAHLVGQTIILSGHSTYIYVIATAPNNFNVDVGLVYSPHPDEQVSALGGIP 138
QY 121 YSQIYGWYRVNFGVIDERLHNRNRYDRYRNLIAPAEDGYRLAGFPDQAWREEPWI 180
Db 139 YSQIYGWYRVHFGVLDQLHNRNGYDRYYSNLDIAPAADGYGLAGFPPEHRAWREEPWI 198
QY 181 HHAPQCGNSRRTITGTCNEETQNLSTIYLYREYQSKVKRQIFSDYQSEVDIYNRIDEL 240
Db 199 HHAPPGCGNAPRSSISNTCDKFTQSLGKFLDEYQSKVKRQIFSGYQSDIDTHNRKDEL 258
Search completed: June 10, 2002, 17:32:05
Job time: 987 sec

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	1304	100.0	240	16	US-09-297-171-1		Sequence 1, Appli
2	1299	99.6	240	6	US-08-256-003-3		Sequence 3, Appli
3	1294	99.2	240	22	US-09-819-917-7		Sequence 7, Appli
4	1287	98.7	259	1	PCT-US99-30747-4		Sequence 4, Appli
5	1287	98.7	259	18	US-09-470-124-4		Sequence 4, Appli
6	1183	90.7	236	6	US-08-256-003-6		Sequence 6, Appli
7	1183	90.7	236	14	US-09-044-696-2		Sequence 2, Appli

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Query Match      100.0%; Score 1304; DB 16; Length 240;
Best Local Similarity 100.0%; Pred. No. 5.5e-137;
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  NGRDLYRADSRPPDEIKRSGGLMPRGHNEYFDRCTOMNINLYDHARGTQTGFVYDDGYV 60
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Db      1  NGRDLYRADSRPPDEIKRSGGLMPRGHNEYFDRCTOMNINLYDHARGTQTGFVYDDGYV 60

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QY 61 STSLSRSAHLAQSILSGYSTYYIVYIATAPNMFNVNDVLGVSPHPYEQEVSALGGIP 120
Db 61 STSLSRSAHLAQSILSGYSTYYIVYIATAPNMFNVNDVLGVSPHPYEQEVSALGGIP 120
QY 121 YSQIYGWYRVNFGVIDERLHRNREYRDYRNINLNIAPAEADGYRLAGPPDQAWREEPWI 180
Db 121 YSQIYGWYRVNFGVIDERLHRNREYRDYRNINLNIAPAEADGYRLAGPPDQAWREEPWI 180
QY 181 HHAPOGCGNSSRTITGDTCTNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIDEL 240
Db 181 HHAPOGCGNSSRTITGDTCTNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIDEL 240

RESULT 2
US-08-256-003-3
; Sequence 3, Application US/08256003
; GENERAL INFORMATION:
; APPLICANT: Domenighini, Mario
; APPLICANT: Rappuoli, Rino
; APPLICANT: Pizza, Mariagrazia
; TITLE OF INVENTION: Immunogenic Detoxified Mutants of
; TITLE OF INVENTION: Cholera Toxin and of the Toxin Lt, Their Preparation and
; TITLE OF INVENTION: Their Use for the Preparation of Vaccines
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: California
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,003
; FILING DATE: 11-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McClung, Barbara G.
; REGISTRATION NUMBER: 33,113
; REFERENCE/DOCKET NUMBER: 0315.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2708
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-256-003-3

Query Match 99.6%; Score 1299; DB 6; Length 240;
Best Local Similarity 99.6%; Pred. No. 2e-136;
Matches 239; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NGDRLRADSRPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVYDDGYV 60
Db 1 NGDRLRADSRPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVYDDGYV 60
QY 61 STSLSRSAHLAQSILSGYSTYYIVYIATAPNMFNVNDVLGVSPHPYEQEVSALGGIP 120
Db 61 STSLSRSAHLAQSILSGYSTYYIVYIATAPNMFNVNDVLGVSPHPYEQEVSALGGIP 120
QY 121 YSQIYGWYRVNFGVIDERLHRNREYRDYRNINLNIAPAEADGYRLAGPPDQAWREEPWI 180
Db 121 YSQIYGWYRVNFGVIDERLHRNREYRDYRNINLNIAPAEADGYRLAGPPDQAWREEPWI 180

QY 181 HHAPOGCGNSSRTITGDTCTNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIDEL 240
Db 181 HHAPOGCGNSSRTITGDTCTNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIDEL 240

RESULT 3
US-09-819-917-7
; Sequence 7, Application US/09819917
; GENERAL INFORMATION:
; APPLICANT: Pizza, Mariagrazia
; APPLICANT: Fontana, Maria Rita
; APPLICANT: Giannelli, Valentina
; APPLICANT: Rappuoli, Rina
; TITLE OF INVENTION: Immunogenic Detoxified Mutants of Cholera Toxin
; FILE REFERENCE: CHIR0312
; CURRENT APPLICATION NUMBER: US/09/819,917
; CURRENT FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 08/981,208
; PRIOR FILING DATE: 1997-12-22
; PRIOR APPLICATION NUMBER: 9513371.6
; PRIOR FILING DATE: 1995-06-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 240
; TYPE: PRT
; ORGANISM: E. coli
US-09-819-917-7

Query Match 99.2%; Score 1294; DB 22; Length 240;
Best Local Similarity 99.2%; Pred. No. 7.3e-136;
Matches 238; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NGDRLRADSRPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVYDDGYV 60
Db 1 NGDRLRADSRPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVYDDGYV 60
QY 61 STSLSRSAHLAQSILSGYSTYYIVYIATAPNMFNVNDVLGVSPHPYEQEVSALGGIP 120
Db 61 STSLSRSAHLAQSILSGYSTYYIVYIATAPNMFNVNDVLGVSPHPYEQEVSALGGIP 120
QY 121 YSQIYGWYRVNFGVIDERLHRNREYRDYRNINLNIAPAEADGYRLAGPPDQAWREEPWI 180
Db 121 YSQIYGWYRVNFGVIDERLHRNREYRDYRNINLNIAPAEADGYRLAGPPDQAWREEPWI 180
QY 181 HHAPOGCGNSSRTITGDTCTNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIDEL 240
Db 181 HHAPOGCGNSSRTITGDTCTNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIDEL 240

RESULT 4
PCT-US99-30747-4
; Sequence 4, Application PC/TUS9930747
; GENERAL INFORMATION:

; APPLICANT: Boyce Thompson Institute for Plant Research at Cor
; TITLE OF INVENTION: Orally Immunogenic Bacterial Enterotoxins Expressed In
; TITLE OF INVENTION: Transgenic Plants
; FILE REFERENCE: 4868/85427
; CURRENT APPLICATION NUMBER: PCT/US99/30747
; CURRENT FILING DATE: 1999-12-22
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:E. coli
; OTHER INFORMATION: heat-labile toxin gene mutagenized to optimize
; OTHER INFORMATION: expression in plants.
PCT-US99-30747-4

Query Match 98.7%; Score 1287; DB 1; Length 259;
Best Local Similarity 98.3%; Pred. No. 5e-135;
Matches 236; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 NGDRLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQNNINLYDHARGTQTGFVYDDGYV 60
DB 20 NGDKLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQNNINLYDHARGTQTGFVYDDGYV 79
QY 61 STSLSRSAHLAQSILSGYSTYIIYVIATAPNMFNVDVGLVYSPHPYEQEVSALGGIP 120
DB 80 STSLSRSAHLAQSILSGYSTYIIYVIATAPNMFNVDVGLVYSPHPYEQEVSALGGIP 139
QY 121 YSIIYGWYRVNFGVIDERLHRNREYDRYRNINLPAEDGYRLAGFPDPHQAAREPWI 180
DB 140 YSIIYGWYRVNFGVIDERLHRNREYDRYRNINLPAEDGYRLAGFPDPHQAAREPWI 199
QY 181 HHAPOCGDSSRITGDTCTNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL 240
DB 200 HHAPOCGDSSRITGDTCTNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL 259

RESULT 5

US-09-470-124-4
; Sequence 4, Application US/09470124
; GENERAL INFORMATION:
; APPLICANT: Mason
; APPLICANT: Arntzen
; TITLE OF INVENTION: Orally Immunogenic Bacterial Enterotoxins Expressed In
; FILE REFERENCE: 4868/84454
; CURRENT APPLICATION NUMBER: US/09/470,124
; CURRENT FILING DATE: 1999-12-24
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:E. coli
; OTHER INFORMATION: heat-labile toxin gene mutagenized to optimize
; OTHER INFORMATION: expression in plants.
US-09-470-124-4

Query Match 98.7%; Score 1287; DB 18; Length 259;
Best Local Similarity 98.3%; Pred. No. 5e-135;
Matches 236; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 NGDRLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQNNINLYDHARGTQTGFVYDDGYV 60
DB 20 NGDKLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQNNINLYDHARGTQTGFVYDDGYV 79
QY 61 STSLSRSAHLAQSILSGYSTYIIYVIATAPNMFNVDVGLVYSPHPYEQEVSALGGIP 120
DB 80 STSLSRSAHLAQSILSGYSTYIIYVIATAPNMFNVDVGLVYSPHPYEQEVSALGGIP 139
QY 121 YSIIYGWYRVNFGVIDERLHRNREYDRYRNINLPAEDGYRLAGFPDPHQAAREPWI 180
DB 140 YSIIYGWYRVNFGVIDERLHRNREYDRYRNINLPAEDGYRLAGFPDPHQAAREPWI 199
QY 181 HHAPOCGDSSRITGDTCTNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL 240
DB 200 HHAPOCGDSSRITGDTCTNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL 259

RESULT 6

US-08-256-003-6
; Sequence 6, Application US/08256003
; GENERAL INFORMATION:
; APPLICANT: Domenighini, Mario
; APPLICANT: Rappuoli, Rino

; APPLICANT: Pizza, Mariagrazia
; TITLE OF INVENTION: Immunogenic Detoxified Mutants of
; TITLE OF INVENTION: Cholera Toxin and of the Toxin Lt, Their Preparation and
; TITLE OF INVENTION: Their Use for the Preparation of Vaccines
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: California
; COUNTRY: USA
; ZIP: 94508-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,003
; FILING DATE: 11-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McClung, Barbara G.
; REGISTRATION NUMBER: 33,113
; REFERENCE/DOCKET NUMBER: 0315.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2708
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-256-003-6

Query Match 90.7%; Score 1183; DB 6; Length 236;
Best Local Similarity 93.3%; Pred. No. 2e-123;
Matches 224; Conservative 2; Mismatches 10; Indels 4; Gaps 2;

QY 1 NGDRLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQNNINLYDHARGTQTGFVYDDGYV 60
DB 1 NGDRLYRADSRPPDEIKRSGGLMPRG-NEYFDRGTQNNINLYDHARGTQTGFVYDDGYV 59
QY 61 STSLSRSAHLAQSILSGYSTYIIYVIATAPNMFNVDVGLVYSPHPYEQEVSALGGIP 120
DB 60 STSLSRSAHLAQSILSGYSTIYIVIA---NMFNVDVSVSPHPYEQEVSALGGIP 116
QY 121 YSIIYGWYRVNFGVIDERLHRNREYDRYRNINLPAEDGYRLAGFPDPHQAAREPWI 180
DB 117 YSIIYGWYRVNFGVIDERLHRNREYDRYRNINLPAEDGYRLAGFPDPHQAAREPWI 176
QY 181 HHAPOCGDSSRITGDTCTNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL 240
DB 177 HHAPOCGDSSRITGDTCTNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL 236

RESULT 7

US-09-044-696-2
; Sequence 2, Application US/09044696
; GENERAL INFORMATION:
; APPLICANT: BARCHELD, GAIL
; APPLICANT: DEL GIUDICE, GIUSEPPE
; APPLICANT: RAPPUOLI, RINO
; TITLE OF INVENTION: DETOXIFIED MUTANTS OF BACTERIAL
; TITLE OF INVENTION: ADP-RIBOSYLATING TOXINS AS PARENTERAL ADJUVANTS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION, INTELLECTUAL PROPERTY -
; ADDRESS: R440
; STREET: P.O. BOX 8097
; CITY: EMERYVILLE

; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/044,696
; FILING DATE: 18-MAR-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 50/041,227
; FILING DATE: 21-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: HARBIN, ALISA A.
; REGISTRATION NUMBER: 33,895
; REFERENCE/DOCKET NUMBER: 1393.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 655-8730
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-044-696-2

Query Match 90.7%; Score 1183; DB 14; Length 236;
Best Local Similarity 93.3%; Pred. No. 2e-123;
Matches 224; Conservative 2; Mismatches 10; Indels 4; Gaps 2;

QY 1 NGDRLYRADSRPDEIKRSGGLMPRGHNEYFDRGTQNMNLYDHARGTQTGFVRYDDGYV 60
Db 1 NGDRLYRADSRPDEIKRFRSLMPRG-NEYFDRGTQNMNLYDHARGTQTGFVRYDDGYV 59

QY 61 STSLRSALHAGQILSGSLTYIYVIATAPNMFNVNDVLGYSPHPYEQEVSALGGIP 120
Db 60 STSLRSALHAGQILSGSLTYIYVIA--NMFNVDVSVSPHPYEQEVSALGGIP 116

QY 121 YSQIYGWYRNFVGVIDERLHRNREYDRYRNLIAPAEDGYRLAGPPDQAWREPWI 180
Db 117 YSQIYGWYRNFVGVIDERLHRNREYDRYRNLIAPAEDGYRLAGPPDQAWREPWI 176

QY 181 HHAPOCGNSRRTITGTCNEETQNLSTIYLYREYQSKVKRQIFSDYQSEVDIYNRIDEL 240
Db 177 HHAPOCGDSRRTITGTCNEETQNLSTIYLYREYQSKVKRQIFSDYQSEVDIYNRIDEL 236

RESULT 8
US-08-360-107-124
; Sequence 124, Application US/08360107
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA

; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,107
; FILING DATE: 20-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8664
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 124:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-360-107-124

Query Match 90.7%; Score 1183; DB 7; Length 254;
Best Local Similarity 93.3%; Pred. No. 2.2e-123;
Matches 224; Conservative 2; Mismatches 10; Indels 4; Gaps 2;

QY 1 NGDRLYRADSRPDEIKRSGGLMPRGHNEYFDRGTQNMNLYDHARGTQTGFVRYDDGYV 60
Db 19 NGDRLYRADSRPDEIKRFRSLMPRG-NEYFDRGTQNMNLYDHARGTQTGFVRYDDGYV 77

QY 61 STSLRSALHAGQILSGSLTYIYVIATAPNMFNVNDVLGYSPHPYEQEVSALGGIP 120
Db 78 STSLRSALHAGQILSGSLTYIYVIA--NMFNVDVSVSPHPYEQEVSALGGIP 134

QY 121 YSQIYGWYRNFVGVIDERLHRNREYDRYRNLIAPAEDGYRLAGPPDQAWREPWI 180
Db 135 YSQIYGWYRNFVGVIDERLHRNREYDRYRNLIAPAEDGYRLAGPPDQAWREPWI 194

QY 181 HHAPOCGNSRRTITGTCNEETQNLSTIYLYREYQSKVKRQIFSDYQSEVDIYNRIDEL 240
Db 195 HHAPOCGDSRRTITGTCNEETQNLSTIYLYREYQSKVKRQIFSDYQSEVDIYNRIDEL 254

RESULT 9
US-08-470-896-114
; Sequence 114, Application US/08470896
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,896
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-470-896-114

Query Match 90.7%; Score 1183; DB 8; Length 254;

Best Local Similarity 93.3%; Pred. No. 2.2e-123;

Matches 224; Conservative 2; Mismatches 10; Indels 4; Gaps 2;

QY 1 NGDRLRADSRPPDEIKRSGGLMPRGHNEYFDRGTQNMNINLYDHARGTQTGFVRYDDGYV 60
|||||
DB 19 NGDRLRADSRPPDEIKRFSRLPRG-NEYFDRGTQNMNINLYDHARGTQTGFVRYDDGYV 77
QY 61 STSLSRSAHLAQOYILSGYSLTIYIVIA---NNFNVDVSYSPHPYQEVSAALGGIP 120
|||||
DB 78 STSLSRSAHLAQOYILSGYSLTIYIVIA---NNFNVDVSYSPHPYQEVSAALGGIP 134
QY 121 YSQIYGYRVNFGVIDERLHRNREYDRYRNINLNIAPAEQYRLAGPPDPHQAWAREPWI 180
|||||
DB 135 YSQIYGYRVNFGVIDERLHRNREYDRYRNINLNIAPAEQYRLAGPPDPHQAWAREPWI 194
QY 181 HHAPOGCGSSRTITGTCNEETQNLSTIYLYREVQSKVKRQIFSDYQSEVDIYNRIDEL 240
|||||
DB 195 HHAPOGCGSSRTITGTCNEETQNLSTIYLYREVQSKVKRQIFSDYQSEVDIYNRIDEL 254

RESULT 10

US-08-471-913-114

Sequence 114, Application US/08471913

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE

TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 209

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,913
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-471-913-114

Query Match 90.7%; Score 1183; DB 8; Length 254;

Best Local Similarity 93.3%; Pred. No. 2.2e-123;

Matches 224; Conservative 2; Mismatches 10; Indels 4; Gaps 2;

QY 1 NGDRLRADSRPPDEIKRSGGLMPRGHNEYFDRGTQNMNINLYDHARGTQTGFVRYDDGYV 60
|||||
DB 19 NGDRLRADSRPPDEIKRFSRLPRG-NEYFDRGTQNMNINLYDHARGTQTGFVRYDDGYV 77
QY 61 STSLSRSAHLAQOYILSGYSLTIYIVIA---NNFNVDVSYSPHPYQEVSAALGGIP 120
|||||
DB 78 STSLSRSAHLAQOYILSGYSLTIYIVIA---NNFNVDVSYSPHPYQEVSAALGGIP 134
QY 121 YSQIYGYRVNFGVIDERLHRNREYDRYRNINLNIAPAEQYRLAGPPDPHQAWAREPWI 180
|||||
DB 135 YSQIYGYRVNFGVIDERLHRNREYDRYRNINLNIAPAEQYRLAGPPDPHQAWAREPWI 194
QY 181 HHAPOGCGSSRTITGTCNEETQNLSTIYLYREVQSKVKRQIFSDYQSEVDIYNRIDEL 240
|||||
DB 195 HHAPOGCGSSRTITGTCNEETQNLSTIYLYREVQSKVKRQIFSDYQSEVDIYNRIDEL 254

RESULT 11

US-08-475-668-114

Sequence 114, Application US/08475668

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA

TITLE OF INVENTION: VIRUS TRANSMISSION

NUMBER OF SEQUENCES: 209

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/475,668

FILING DATE: 07-JUN-1995

CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-026
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-475-668-114

Query Match 90.7%; Score 1183; DB 8; Length 254;
Best Local Similarity 93.3%; Pred. No. 2.2e-123;
Matches 224; Conservative 2; Mismatches 10; Indels 4; Gaps 2;
QY 1 NGDRLYRADSRPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTGTGFVRYDDGYV 60
DB 19 NGDRLYRADSRPDEIKRFRSLMPRG-NEYFDRGTQMNINLYDHARGTGTGFVRYDDGYV 77
QY 61 STSLSLSAHLAQSGILSGYSTIYIYVIATAPNMFNVNDVLGYSPHPYEQEVSALGGIP 120
DB 78 STSLSLSAHLAQGYILSGYSLTIYIVIA---NMFNVDVISVSPHPYEQEVSALGGIP 134
QY 121 YSQIYGWYRVNFGVIDERLHRNREYRDYRNINLPAEDGYRLAGFPDPDQAWREEPWI 180
DB 135 YSQIYGWYRVNFGVIDERLHRNREYRDYRNINLPAEDGYRLAGFPDPDQAWREEPWI 194
QY 181 HHAPOCGGSSRTITGTCNEETQNLSTIYLYREYQSKVKRQIFSDYQSEVDIYNRIDEL 240
DB 195 HHAPOCGGSSRTITGTCNEETQNLSTIYLYREYQSKVKRQIFSDYQSEVDIYNRIDEL 254

RESULT 12
US-08-484-223-114
Sequence 114, Application US/08484223
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-484-223-114

Query Match 90.7%; Score 1183; DB 8; Length 254;
Best Local Similarity 93.3%; Pred. No. 2.2e-123;
Matches 224; Conservative 2; Mismatches 10; Indels 4; Gaps 2;
QY 1 NGDRLYRADSRPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTGTGFVRYDDGYV 60
DB 19 NGDRLYRADSRPDEIKRFRSLMPRG-NEYFDRGTQMNINLYDHARGTGTGFVRYDDGYV 77
QY 61 STSLSLSAHLAQSGILSGYSTIYIYVIATAPNMFNVNDVLGYSPHPYEQEVSALGGIP 120
DB 78 STSLSLSAHLAQGYILSGYSLTIYIVIA---NMFNVDVISVSPHPYEQEVSALGGIP 134
QY 121 YSQIYGWYRVNFGVIDERLHRNREYRDYRNINLPAEDGYRLAGFPDPDQAWREEPWI 180
DB 135 YSQIYGWYRVNFGVIDERLHRNREYRDYRNINLPAEDGYRLAGFPDPDQAWREEPWI 194
QY 181 HHAPOCGGSSRTITGTCNEETQNLSTIYLYREYQSKVKRQIFSDYQSEVDIYNRIDEL 240
DB 195 HHAPOCGGSSRTITGTCNEETQNLSTIYLYREYQSKVKRQIFSDYQSEVDIYNRIDEL 254

RESULT 13
US-08-484-223A-114
Sequence 114, Application US/08484223A
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:

; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-485-546A-114

Query Match		90.7%	Score 1183;	DB 8;	Length 254;
Best Local Similarity		93.3%	Pred. No. 2.2e-123;		
Matches	224;	Conservative	2;	Mismatches	10;
				Indels	4;
				Gaps	2;
Qy	1	NGDRLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTOMNINLYDHARGTQTGFVRYDDGYV	60		
Db	19	NGDRLYRADSRPPDEIKRFRSLMPRG-NEYFDRGTOMNINLYDHARGTQTGFVRYDDGYV	77		
Qy	61	STSLSLSAHLAQSIILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIP	120		
Db	78	STSLSLSAHLAQSIILSGYSLTIYIVIA---NMFNVDVISYSPHPYEQEVSALGGIP	134		
Qy	121	YSQIYGWYRVNFGVIDERLHNRNREYRDYRNLNIAPAEDGYRLAGFPPDQAWREEPWI	180		
Db	135	YSQIYGWYRVNFGVIDERLHNRNREYRDYRNLNIAPAEDGYRLAGFPPDQAWREEPWI	194		
Qy	181	HHAPQCGNSRRTTGTCTCNEETONLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIDEL	240		
Db	195	HHAPQCGDSRRTTGTCTCNEETONLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIDEL	254		

Search completed: June 10, 2002, 17:35:18
Job time: 210 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 10, 2002, 17:32:08 ; Search time 15.77 Seconds
(without alignments)
1167.219 Million cell updates/sec

Title: US-09-297-171-1
Perfect score: 1304
Sequence: 1 NGDRLYRADSRPPDEIKRSG.....QIFSDYQSEVDIYNRIRDEL 240

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 233302 seqs, 76696041 residues

Total number of hits satisfying chosen parameters: 233302

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New.*
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US05_NEW_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Préd. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1304	100.0	240	5	US-09-528-682-1
2	1088	83.4	382	5	US-09-809-033A-3
3	1084	83.1	382	5	US-09-809-033A-4
4	89	6.8	1119	5	US-09-540-209B-9958
5	88	6.7	1008	5	US-09-540-209B-8074
6	86	6.6	423	7	US-60-360-039-22895
7	84	6.4	875	7	US-60-360-039-17808
8	82	6.3	1095	7	US-60-360-039-4059
9	81.5	6.2	676	7	US-60-360-039-4730
10	81.5	6.2	680	7	US-60-360-039-7489
11	81	6.2	256	5	US-09-513-345-5
12	81	6.2	256	6	US-10-109-551-2
13	81	6.2	256	6	US-10-109-551-10
14	81	6.2	263	1	PCT-US02-13346-3
15	81	6.2	264	5	US-09-602-775C-26
16	81	6.2	264	6	US-10-096-080-21
17	80	6.1	254	5	US-09-513-345-3
18	80	6.1	254	5	US-09-602-775C-30
19	80	6.1	254	6	US-10-096-080-26
20	80	6.1	1087	5	US-09-540-209B-7962
21	79.5	6.1	207	1	PCT-US02-09921-630
22	79	6.1	256	6	US-10-109-551-6
23	79	6.1	256	6	US-10-109-551-8
24	78.5	6.0	433	7	US-60-360-039-11030
25	78	6.0	255	1	PCT-US02-13346-4
26	78	6.0	256	6	US-10-109-551-4

27	78	6.0	475	7	US-60-360-039-5679	Sequence 5679, Ap
28	77.5	5.9	430	5	US-09-540-209B-6743	Sequence 6743, Ap
29	77.5	5.9	948	5	US-09-540-209B-10195	Sequence 10195, A
30	77	5.9	254	6	US-10-096-080-28	Sequence 28, Appl
31	77	5.9	436	7	US-60-360-039-18195	Sequence 18195, A
32	77	5.9	479	7	US-60-360-039-18842	Sequence 18842, A
33	77	5.9	720	7	US-60-360-039-2848	Sequence 2848, Ap
34	77	5.9	989	5	US-09-935-625-7548	Sequence 7548, Ap
35	77	5.9	989	5	US-09-935-625-28206	Sequence 28206, A
36	77	5.9	994	5	US-09-935-625-7547	Sequence 7547, Ap
37	77	5.9	994	5	US-09-935-625-28205	Sequence 28205, A
38	77	5.9	1006	5	US-09-935-625-28204	Sequence 28204, A
39	77	5.9	1006	5	US-09-935-625-8784	Sequence 8784, Ap
40	77	5.9	1031	5	US-09-935-625-29529	Sequence 29529, A
41	77	5.9	1031	5	US-09-935-625-8783	Sequence 8783, Ap
42	77	5.9	1043	5	US-09-935-625-29528	Sequence 29528, A
43	77	5.9	1043	5	US-09-540-209B-6297	Sequence 6297, Ap
44	76.5	5.9	434	5	PCT-US02-13142-3075	Sequence 3075, Ap
45	76.5	5.9	476	1		

ALIGNMENTS

RESULT 1
US-09-528-682-1
; Sequence 1, Application US/09528682
; GENERAL INFORMATION:
; APPLICANT: Pizsa, Mariagrazia
; APPLICANT: Giuliani, Marzia M
; APPLICANT: Rappuoli, Rino
; TITLE OF INVENTION: IMMUNOGENIC DETOXIFIED MUTANT E. COLI LT-A-TOXIN
; FILE REFERENCE: 2302-0342.10
; CURRENT APPLICATION NUMBER: US/09/528,682
; CURRENT FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: PCT/IB97/01440
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: 09/297,171
; PRIOR FILING DATE: 1999-04-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-528-682-1

Query Match 100.0%; Score 1304; DB 5; Length 240;
Best Local Similarity 100.0%; Pred. No. 3.9e-117;
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NGDRLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQNMNLYDHARGTQTGFVRYDDGYV 60
|||||

Db 1 NGDRLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQNMNLYDHARGTQTGFVRYDDGYV 60
|||||

Qy 61 STSLSRSAHLACGSILSGSYTYIYVIATAPNMFNVNVLGVSPHPYQEVYSALGGIP 120
|||||

Db 61 STSLSRSAHLACGSILSGSYTYIYVIATAPNMFNVNVLGVSPHPYQEVYSALGGIP 120
|||||

Qy 121 YSQIYGYRWYVNFVYDRLHNRREYRDYRNLNIAPAEDGYRLAGFPDQAWREPEWI 180
|||||

Db 121 YSQIYGYRWYVNFVYDRLHNRREYRDYRNLNIAPAEDGYRLAGFPDQAWREPEWI 180
|||||

Qy 181 HHAPOCGNSRRTITGTCNEETONLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL 240
|||||

Db 181 HHAPOCGNSRRTITGTCNEETONLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL 240
|||||

RESULT 2
US-09-809-033A-3
; Sequence 3, Application US/09809033A
; GENERAL INFORMATION:

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 10, 2002, 17:32:33 ; Search time 29.32 Seconds
(without alignments)
909.199 Million cell updates/sec

Title: US-09-297-171-1
Perfect score: 240
Sequence: 1 NGDRLYRADSRPPDEIKRSG.....QIFSDYQSEVDIYNRDEL 240

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0
Searched: 747574 seqs, 111073796 residues

Word size : 8
Total number of hits satisfying chosen parameters: 82

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :	A_Geneseq_032802.*
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2:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
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4:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
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6:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.*
7:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.*
8:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.*
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21:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	240	100.0	258	6 AAP50190	Sequence encoded b
2	184	76.7	259	21 AAY96646	Plant-optimized E.
3	184	76.7	259	21 AAY96648	Plant-optimized E.
4	179	74.6	258	6 AAP50191	Sequence encoded b
5	177	73.8	382	22 AAU00506	E. coli heat-lab
6	128	53.3	380	22 AAU00507	E. coli heat-lab
7	125	52.1	259	21 AAY96647	Synthetic E. coli
8	125	52.1	259	21 AAY96650	Plant-optimized E.
9	116	48.3	259	21 AAY96649	Plant-optimized E.
10	116	48.3	259	21 AAY96651	Plant-optimized E.
11	111	46.2	240	19 AAW65074	E. coli LT-A prote

12	99	41.2	240	19 AAW65075	E. coli LT-A mutan
13	86	35.8	236	14 AAR44016	"Lys-63" E.coli he
14	86	35.8	236	14 AAR44017	"Lys-97" E.coli he
15	86	35.8	236	14 AAR44018	"Tyr-97" E.coli he
16	86	35.8	236	14 AAR38728	E.coli heat labile
17	86	35.8	236	14 AAR38730	"Asp-53" E.coli he
18	86	35.8	236	14 AAR38731	"Glu-53" E.coli he
19	86	35.8	236	14 AAR38732	"Tyr-53" E.coli he
20	86	35.8	237	20 AAW67772	E. coli heat labil
21	86	35.8	254	22 AAU14105	Peptide sequence f
22	84	35.0	236	14 AAR44020	"Lys-104" E.coli h
23	84	35.0	236	14 AAR44021	"Asp-104" E.coli h
24	84	35.0	236	14 AAR44022	"Ser-104" E.coli h
25	82	34.2	236	14 AAR44023	"Ser-106" E.coli h
26	81	33.8	236	14 AAR44024	"Glu-107" E.coli h
27	74	30.8	236	14 AAR44025	"Glu-114" E.coli h
28	74	30.8	236	14 AAR44026	"Lys-114" E.coli h
29	26	10.8	240	14 AAR44027	Asn-107 cholera to
30	26	10.8	240	14 AAR44028	Lys-63 cholera tox
31	26	10.8	240	14 AAR44029	Lys-97 cholera tox
32	26	10.8	240	14 AAR44030	Ser-106 cholera to
33	26	10.8	240	14 AAR44031	Ser-110 cholera to
34	26	10.8	240	14 AAR44032	Ala-112 cholera to
35	26	10.8	240	14 AAR44033	Glu-114 cholera to
36	26	10.8	240	14 AAR38729	Cholera toxin subu
37	26	10.8	240	19 AAW80809	Amino acid sequenc
38	26	10.8	240	19 AAW80807	Cholera toxin subu
39	26	10.8	240	20 AAW67773	Plant-optimized V.
40	26	10.8	258	21 AAY96653	Plant-optimized mu
41	26	10.8	258	21 AAY96654	Plant-optimized mu
42	26	10.8	258	21 AAY96655	Plant-optimized mu
43	26	10.8	258	21 AAY96656	Plant-optimized mu
44	26	10.8	258	22 AAG65991	Cholera toxin A su
45	25	10.4	258	12 AAR13117	Cholera toxin Al f

ALIGNMENTS

RESULT 1	
AAP50190	
ID AAP50190 standard; Protein; 258 AA.	
XX	
AC AAP50190;	
XX	
DT 30-OCT-1991 (first entry)	
XX	
DE Sequence encoded by the pig scours heat labile toxin (LT) LTA gene.	
XX	
KW Pig scours vaccine; toxin; diarrhoea.	
XX	
OS E.coli NCIB 11932.	
XX	
PN EP145486-A.	
XX	
PD 19-JUN-1985.	
XX	
PF 12-DEC-1984; 84EP-0308620.	
XX	
PR 12-DEC-1983; 83GB-0033131.	
XX	
PA (GLAX) GLAXO GROUP LTD.	
XX	
PI Hayes MV, Harford S, Ross GW;	
XX	
DR WPI: 1985-148358/25.	
DR N-PSDB; AAN50205.	
XX	
PT New toxoid as inactivated form of toxin for use in vaccines - is	
PT obtd. from organism transformed by gene	
XX	
PS Disclosure; Fig 1; 61pp; English.	
XX	

CC AAN50205 is the gene sequence of the natural LTA gene. The LTA gene of
CC the site directed mutant SDM1 (see AAN50206) is inactive. The
CC inventors claim a vaccine prepn. active against pig scours which
CC contains an inactivated LTA component, together with additional K88
CC antigens opt. with whole cells comprising the antigens or contg. the
CC inactivated LTA.
XX
SQ Sequence 258 AA;

Query Match 100.0%; Score 240; DB 6; Length 258;
Best Local Similarity 100.0%; Pred. No. 1.2e-238; Indels 0; Gaps 0;
Matches 240; Conservative 0; Mismatches 0;

Qy 1 NGDRLRADSRPPDEIKRSGGLMPRGHNEYFDRGTOMNINLYDHARGTGTGFVRYDDGYV 60
Db 19 ngdrlradsrppdeikrsgglmpgrhneyfdrgtqmninlydharqtgtgfvyddgyv 78
Qy 61 STSLSLRSLAHLAGOSILSGYSTYYIVYIATAPNMFNVDVGVSPHPYEQEVSALGGIP 120
Db 79 stslslrsahlagosilsgystyyiviatapnmfnvndvlgvysphpyeqevsalggip 138
Qy 121 YSQIYGWYRVNFGVIDERLHRNREYDRYRNINLAPAEQYRLAGFPDPDQAWREPEWI 180
Db 139 ysqiygwyrvnfgviderlhrnreydryrnlinaeapgedyrlagfpdpdqawreepwi 198
Qy 181 HHAPQGCNSTRITGDTCEETONLSTIYLREYQSKVKQIFSDYQSEVDIYNRIDEL 240
Db 199 hhapqgcnsrtitgdtcneetnlslylreyqskvkqifsdysqevdiynrirdel 258

RESULT 2
AAY96646
ID AAY96646 standard; Protein; 259 AA.
XX AAY96646;
AC AAY96646;
XX
DT 26-SEP-2000 (first entry)
DE Plant-optimized E. coli heat labile toxin A subunit.
KW Heat-labile toxin; LT-A; LT-B; mutant; transgenic plant; vaccine; oral;
KW adjuvant; anti-bacterial.
XX Escherichia coli.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..18
FT /label= signal_peptide
FT Protein 19..259
FT /label= mature_protein
XX
PN WO200037609-A2.
XX
XX 29-JUN-2000.
XX
XX 22-DEC-1999; 99WO-US30747.
XX
XX 22-DEC-1998; 98US-0113507.
XX
XX (BOYC-) BOYCE THOMPSON INST PLANT RES.
PA (MASO/) MASON H S.
PA (ARNT/) ARNTZEN C J.
XX
PI Mason HS, Arntzen CJ;
XX
XX WPI; 2000-442653/38.
DR N-PSDB; AAA51106.
XX
XX New polynucleotides encoding LT-A or CT-A polypeptides for the
PT transformation of plant cells, useful in immunogenic compositions to
PT elicit immune responses in animals

XX Example 1; Fig 1; 103pp; English.
PS This synthetic Escherichia coli heat-labile toxin (LT) A subunit (LT-A)
XX is encoded by a plant-codon optimized cDNA. The cDNA sequence contains
CC plant-preferred codons and eliminates sequence motifs associated with
CC spurious mRNA processing. A single codon insertion (GTG encoding valine)
CC was made to accommodate the creation of a NcoI restriction site around the
CC initiator methionine codon. Novel polynucleotides encode a mutant LT-A
CC polypeptide or a mutant Vibrio cholerae cholera toxin (CT) A subunit
CC (CT-A) polypeptide, which have reduced enzyme activity as compared to the
CC wild-type LT-A or CT-A polypeptide and where at least one of the codons
CC is altered to a plant preferred codon. The polynucleotide further
CC comprises a nucleic acid sequence encoding LT B subunit (LT-B) or a CT B
CC subunit (CT-B). The polynucleotides are useful for the transformation of
CC plant cells for the production of transgenic plants to produce edible
CC vaccines, especially oral vaccines in transgenic plants for the
CC prophylactic or therapeutic treatment against E. coli or V. cholerae. The
CC mutant polypeptides are also useful as adjuvants.
XX
SQ Sequence 259 AA;

Query Match 76.7%; Score 184; DB 21; Length 259;
Best Local Similarity 100.0%; Pred. No. 5.4e-181;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LYRADSRPPDEIKRSGGLMPRGHNEYFDRGTOMNINLYDHARGTGTGFVRYDDGYVSTSL 64
Db 24 lyradsrppdeikrsgglmpgrhneyfdrgtqmninlydharqtgtgfvyddgyvstsl 83
Qy 65 SLRSLAHLAGOSILSGYSTYYIVYIATAPNMFNVDVGVSPHPYEQEVSALGGIPYSQI 124
Db 84 slrsahlagosilsgystyyiviatapnmfnvndvlgvysphpyeqevsalggipysqi 143
Qy 125 YGWYRVNFGVIDERLHRNREYDRYRNINLAPAEQYRLAGFPDPDQAWREPEWIHHAP 184
Db 144 ygwyrvnfgviderlhrnreydryrnlinaeapgedyrlagfpdpdqawreepwhhap 203
Qy 185 QGCG 188
Db 204 qgcg 207

RESULT 3
AAY96648
ID AAY96648 standard; Protein; 259 AA.
XX
XX AAY96648;
AC AAY96648;
XX
DT 26-SEP-2000 (first entry)
DE Plant-optimized E. coli LT-A G192 mutant.
XX
XX Heat-labile toxin; LT-A; LT-B; mutant; transgenic plant; vaccine; oral;
KW adjuvant; anti-bacterial; R192G.
XX
XX Escherichia coli.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= signal_peptide
FT Protein 20..259
FT /label= mature_protein
FT Misc-difference 211
FT /label= R192G
FT /note= "Wild-type arginine is replaced by glycine"
XX
XX WO200037609-A2.
PN
XX 29-JUN-2000.
PD
XX

PF 22-DEC-1999; 99WO-US30747.
XX
PR 22-DEC-1998; 98US-0113507.
XX
PA (BOYC-) BQYCE THOMPSON INST PLANT RES.
PA (MASO/) MASON H S.
PA (ARNT/) ARNTZEN C J.
XX
PI Mason HS, Arntzen CJ;
XX
XX WPI; 2000-442653/38.
DR N-PSDB; AAA51544.
XX
XX New polynucleotides encoding LT-A or CT-A polypeptides for the
PT transformation of plant cells, useful in immunogenic compositions to
PT elicit immune responses in animals
XX
XX Example 3; Page -: 103pp; English.
XX
CC This is mutant R192G Escherichia coli heat-labile toxin (LT) A subunit
CC (LT-A). The wild-type arginine was replaced with glycine at residue 192
CC of the mature protein, which was caused by a codon change of TCC to AAG
CC in the coding sequence. The sequence contains plant-preferred codons and
CC eliminates sequence motifs associated with spurious mRNA processing. A
CC single codon insertion (GTG encoding valine) was made to accommodate the
CC creation of a NcoI restriction site around the initiator methionine
CC codon. Novel polynucleotides encode a mutant LT-A polypeptide or a
CC mutant Vibrio cholerae cholera toxin (CT) A subunit (CT-A) polypeptide,
CC which have reduced enzyme activity as compared to the wild-type LT-A or
CC CT-A polypeptide and where at least one of the codons is altered to a
CC plant preferred codon. The polynucleotide further comprises a nucleic
CC acid sequence encoding LT B subunit (LT-B) or a CT B subunit (CT-B). The
CC polynucleotides are useful for the transformation of plant cells for the
CC production of transgenic plants to produce edible vaccines, especially
CC oral vaccines in transgenic plants for the prophylactic or therapeutic
CC treatment against E. coli or V. cholerae. The mutant polypeptides are
CC also useful as adjuvants.
CC NB: This sequence does not appear in the specification, it was made from
CC the wild type sequence shown in AAY96647, which appears in Figure 1.
XX
SQ Sequence 259 AA;

Query Match 76.7%; Score 184; DB 21; Length 259;
Best Local Similarity 100.0%; Pred. No. 5.4e-181; Mismatches 0; Indels 0; Gaps 0;
Matches 184; Conservative 0;

Qy 5 LYRADSRPPDEIKRSGGLMPRGHNEYFDRGTMNINLYDHARGTQTGFVRYDDGVVSTSL 64
Db 24 lyradsrppdeikrsgglmpRGHNEYfdrgtqminlydhargtqtgfvryddgvvstsl 83

Qy 65 SLRSAHLAQSILSGYSTYYIVYIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIPYSQI 124
Db 84 slrsahlagqsilsgystyyiviatapnmfnvndvlgvysphpyeqevsalggipysq1 143

Qy 125 YGWRVNVFGVIDERLHRNREYDRYRNINLNTAPADGVRLAGFPDPHQAWREEPWIHAP 184
Db 144 ygwrnvfnvfgviderlhrnreydryrnrlnlntapadgyrlagfpdpdqawreepwihap 203

Qy 185 QGCG 188
Db 204 qgcg 207

RESULT 4
AAP50191
ID AAP50191 standard; Protein; 258 AA.
XX
AC AAP50191;
XX
DT 30-OCT-1991 (first entry)
XX
DE Sequence encoded by the pig scours heat labile toxin (LT) LTA gene

DE of the site directed mutant SDM1.
XX Pig scours vaccine; toxin; diarrhoea.
XX
XX E.coli NCIB 11932.
XX
XX Key Location/Qualifiers
FT Misc-difference 79 /note= "Ser in native SQ"
XX
XX EPI45486-A.
XX
XX 19-JUN-1985.
XX
XX 12-DEC-1984; 84EP-0308620.
XX
XX 12-DEC-1983; 83GB-0033131.
XX
XX (GLAX) GLAXO GROUP LTD.
XX
XX Hayes MV, Harford S, Ross GW;
PI
XX WPI; 1985-148358/25.
DR N-PSDB; AAN50206.
XX
XX New toxoid as inactivated form of toxin for use in vaccines - is
PT obtd. from organism transformed by gene
XX
XX Example; Fig 2; 61pp; English.
XX
XX AAN50205 is the gene sequence of the natural LTA gene. The LTA gene of
CC the site directed mutant SDM1 (see AAN50206) is inactive. The
CC inventors claim a vaccine prepn. active against pig scours which
CC contains an inactivated LTA component, together with additional K88
CC antigens opt. with whole cells comprising the antigens or contg. the
CC inactivated LTA.
XX
XX Sequence 258 AA;

Query Match 74.6%; Score 179; DB 6; Length 258;
Best Local Similarity 100.0%; Pred. No. 7.6e-176;
Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 62 TSLSRSHLAGQSILSGYSTYYIVYIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIPY 121
Db 80 tslsrshlagqsilsgystyyiviatapnmfnvndvlgvysphpyeqevsalggipy 139

Qy 122 SQIYGWRVNVFGVIDERLHRNREYDRYRNINLNTAPADGVRLAGFPDPHQAWREEPWIH 181
Db 140 sqlygwrnvfnvfgviderlhrnreydryrnrlnlntapadgyrlagfpdpdqawreepwih 199

Qy 182 HAPQCGNSSRTITGDTCTNEETQNLSTIYLRYSQKVRQIFSDYQSEVDIYNRIRDEL 240
Db 200 hapqcgnsrrtittgdtcneetqnlstilyrsgskvrqifsdysqsevdynrirdel 258

RESULT 5
AAU00506
ID AAU00506 standard; Protein; 382 AA.
XX
AC AAU00506;
XX
XX 29-AUG-2001 (first entry)
XX
XX E. coli heat-labile enterotoxin (LT) mutant LTS63Y.
XX
XX Heat-labile enterotoxin; LT; LTS63Y; Ltgell10/112; mutant;
KW detoxified and immunologically active protein; ADP-ribosylation; Gs;
KW endotoxin; diarrhoea; mutein.
XX
XX Escherichia coli strain K88ac.
OS Synthetic.

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XX FH Key Location/Qualifiers
FT Misc_feature 7
FT /note= "Important residue for enzymatic activity"
FT Misc_feature 44
FT /note= "Important residue for enzymatic activity"
FT Region 58..72
FT /note= "Forms the NAD-binding site"
FT Misc_feature 61
FT /note= "Important residue for enzymatic activity"
FT Misc-difference 63
FT /note= "Substitution of wild type Ser to Tyr"
FT Misc_feature 110
FT /note= "Important residue for enzymatic activity"
FT Misc_feature 112
FT /note= "Important residue for enzymatic activity"
FT Misc-difference 259
FT /note= "Encoded by TG"
XX
XX WO200119998-Al.
XX
XX 22-MAR-2001.
XX
XX 15-SEP-1999; 99WO-KR00555.
XX
XX 15-SEP-1999; 99WO-KR00555.
XX
XX (MOGA-) MOGAM BIOTECHNOLOGY RES INST.
XX
XX Park EJ, Kim JS, Chang J, Yum J, Chung S;
XX
XX WPI; 2001-281524/29.
XX
XX N-PSDB; AAS01506.
XX
XX New detoxified mutants of Escherichia coli heat-labile enterotoxin
XX useful as vaccine for preventing and treating diarrhoea, and as adjuvant
XX for antibody production .
XX
XX Claim 2; Page 39-41; 48pp; English.
XX
XX The present sequence represents Escherichia coli heat-labile
XX enterotoxin (LT) mutant LTS63Y and Ldell10/112 (AAU00507)
XX are two novel detoxified and immunologically active proteins (LT
XX mutants) derived by site-directed mutagenesis of the A1 subunit of wild
XX type LT. The substitution of Ser to Tyr at position 63 in LTS63Y blocks
XX NAD-binding. Deletion of Glu residues at positions 110 and 112 in
XX Ldell10/112 eliminate the enzymatic activity of LT. The A1 subunit of
XX wild type LT catalyses ADP-ribosylation of Gs, a GTP-binding protein that
XX regulates cAMP levels. The resulting increase in cAMP is the cause of
XX diarrhoea in humans and animals e.g. pigs. The mucosal immunogenicities
XX of mutant heat-labile endotoxins LTS63Y and Ldell10/112 were tested.
XX Groups of mice were immunised with LTS623Y or Ldell10/112. The control
XX faecal antibody titres to LT were determined. The results showed that
XX mice immunised with LTS63Y or Ldell10/112 contained high and
XX comparable level of anti-LT antibodies in sera and faecal extracts
XX compared with those immunised with wild-type LT. The LT mutants are
XX useful as a vaccine for preventing and treating diarrhoea and as an
XX adjuvant for antibody production.
XX
XX Sequence 382 AA;

Query Match 73.8%; Score 177; DB 22; Length 382;
Best Local Similarity 100.0%; Pred. No. 1.2e-173;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 LLSRAHLAQSILSGYSTYIYVIATAPNMFNVNDVLGYSPHPYEQEVSALGGIPYSQ 123
Db 82 LLSRAHLAQSILSGYSTYIYVIATAPNMFNVNDVLGYSPHPYEQEVSALGGIPYSQ 141
QY 124 IYGYRYNFGVIDERLHRNREYDRYRNINIAPAEDGYLAGFPDPHQWREPWIIHA 193

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Db 142 IYGYRYNFGVIDERLHRNREYDRYRNINIAPAEDGYLAGFPDPHQWREPWIIHA 201
QY 184 POCGSSRRITGDTQNEETNLSTIYLRYSQSKVKRQIESDYQSEVDIYNRIDEL 240
Db 202 PQCGRSSRRITGDTQNEETNLSTIYLRYSQSKVKRQIESDYQSEVDIYNRIDEL 258

RESULT 6
AAU00507
ID AAU00507 standard; Protein; 380 AA.
XX
XX AAU00507;
XX
XX 29-AUG-2001 (first entry)
XX
XX E. coli heat-labile enterotoxin (LT) mutant Ldell10/112.
XX
XX Heat-labile enterotoxin; LT; LTS63Y; Ldell10/112; mutant;
XX detoxified and immunologically active protein; ADP-ribosylation; Gs;
XX endotoxin; diarrhoea; mutein.
XX
XX Escherichia coli strain K88ac.
XX Synthetic.
XX
XX Key Location/Qualifiers
FT Misc_feature 7
FT /note= "Important residue for enzymatic activity"
FT Misc_feature 44
FT /note= "Important residue for enzymatic activity"
FT Region 58..72
FT /note= "Forms the NAD-binding site"
FT Misc_feature 61
FT /note= "Important residue for enzymatic activity"
FT Misc-difference 257
FT /note= "Encoded by TG"
XX
XX WO200119998-Al.
XX
XX 22-MAR-2001.
XX
XX 15-SEP-1999; 99WO-KR00555.
XX
XX 15-SEP-1999; 99WO-KR00555.
XX
XX (MOGA-) MOGAM BIOTECHNOLOGY RES INST.
XX
XX Park EJ, Kim JS, Chang J, Yum J, Chung S;
XX
XX WPI; 2001-281524/29.
XX
XX N-PSDB; AAS01506.
XX
XX New detoxified mutants of Escherichia coli heat-labile enterotoxin
XX useful as vaccine for preventing and treating diarrhoea, and as adjuvant
XX for antibody production .
XX
XX Claim 6; Page 42-44; 48pp; English.
XX
XX The present sequence represents Escherichia coli heat-labile
XX enterotoxin (LT) mutant Ldell10/112. LTS63Y (AAU00506) and Ldell10/112
XX are two novel detoxified and immunologically active proteins (LT
XX mutants) derived by site-directed mutagenesis of the A1 subunit of wild
XX type LT. The substitution of Ser to Tyr at position 63 in LTS63Y blocks
XX NAD-binding. Deletion of Glu residues at positions 110 and 112 in
XX Ldell10/112 eliminate the enzymatic activity of LT. The A1 subunit of
XX wild type LT catalyses ADP-ribosylation of Gs, a GTP-binding protein that
XX regulates cAMP levels. The resulting increase in cAMP is the cause of
XX diarrhoea in humans and animals e.g. pigs. The mucosal immunogenicities
XX of mutant heat-labile endotoxins LTS63Y and Ldell10/112 were tested.
XX Groups of mice were immunised with LTS623Y or Ldell10/112. The control
XX faecal antibody titres to LT were determined. The results showed that
XX mice immunised with LTS63Y or Ldell10/112 contained high and
XX comparable level of anti-LT antibodies in sera and faecal extracts

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PD 29-JUN-2000.
XX
PF 22-DEC-1999; 99WO-US30747.
XX
XX 22-DEC-1998; 98US-0113507.
XX
XX (BOYC-) BOYCE THOMPSON INST PLANT RES.
PA (MASO/) MASON H S.
PA (ARNT/) ARNTZEN C J.
XX
XX Mason HS, Arntzen CJ;
PI WPI; 2000-442653/38.
XX
XX New polynucleotides encoding LT-A or CT-A polypeptides for the
PT transformation of plant cells, useful in immunogenic compositions to
PT elicit immune responses in animals
XX
XX Example 5; Page -: 103pp; English.
XX
XX This is Escherichia coli heat-labile toxin (LT) A subunit (LT-A) double
CC mutant S3kR192G. The wild-type serine was replaced with lysine at
CC residue 63 and wild-type arginine was replaced with glycine at residue
CC 192 of the mature protein. The coding sequence contains plant-preferred
CC codons and eliminates sequence motifs associated with spurious mRNA
CC processing. A single codon insertion (GTG encoding valine) was made to
CC accommodate the creation of a NcoI restriction site around the initiator
CC methionine codon. Novel polynucleotides encode a mutant LT-A polypeptide
CC or a mutant Vibrio cholerae cholera toxin (CT) A subunit (CT-A)
CC polypeptide, which have reduced enzyme activity as compared to the
CC wild-type LT-A or CT-A polypeptide and where at least one of the codons
CC is altered to a plant preferred codon. The polynucleotide further
CC comprises a nucleic acid sequence encoding LT B subunit (LT-B) or a CT B
CC subunit (CT-B). The polynucleotides are useful for the transformation of
CC plant cells for the production of transgenic plants to produce edible
CC vaccines, especially oral vaccines in transgenic plants for the
CC prophylactic or therapeutic treatment against E. coli or V. cholerae.
CC The mutant polypeptides are also useful as adjuvants.
CC Note: This sequence does not appear in the specification. It was
CC constructed from the wild type LT-A shown in AAY96646 which is given
CC in Figure 1 of the specification.
XX
XX Sequence 259 AA;
SQ
Query Match 52.1%; Score 125; DB 21; Length 259;
Best Local Similarity 100.0%; Pred. No. 2.9e-120;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 64 LSLRSALGAGSILSGYSTYIYVIATAPNMFNVDVGVSPHPYEQEVSALGGIPYSQ 123
DB 83 lsrsahlaggsilsgystyiyviatcapmfnvndvlgvysphpyeqevsalggipysq 142
QY 124 IYGWYRVNFGVIDERLHNRREYDRYRNINLAPAEADGYRLAGFPDPDQAWREEPWIHHA 183
DB 143 iygwrvnfgviderlhnrreaydrdryrnlinaapaedgyrlagfpdpdqawreepwihha 202
QY 184 PQCGG 188
DB 203 pqgcg 207
RESULT 9
AAY96649
ID AAY96649 standard; Protein: 259 AA.
XX
XX AAY96649;
XX AC
XX 26-SEP-2000 (first entry)
XX
XX Plant-optimized E. coli LT-A R72 mutant.
XX
XX Heat-labile toxin; LT-A; LT-B; mutant; transgenic plant; vaccine; oral;
KW adjuvant; "anti-bacterial; A72R.
XX
OS Escherichia coli.
OS Synthetic.
XX
XX Key Location/Qualifiers
XX Peptide 1..19
XX Protein /label= signal_peptide
XX /label= mature_protein
XX Misc-difference 91
XX /label= A72R
XX /note= "Wild type alanine is replaced by arginine"
XX
XX WO200037609-A2.
XX
XX 29-JUN-2000.
XX
XX 22-DEC-1999; 99WO-US30747.
XX
XX 22-DEC-1998; 98US-0113507.
XX
XX (BOYC-) BOYCE THOMPSON INST PLANT RES.
PA (MASO/) MASON H S.
PA (ARNT/) ARNTZEN C J.
XX
XX Mason HS, Arntzen CJ;
PI WPI; 2000-442653/38.
XX
XX N-PSDB; AAA51545.
XX
XX New polynucleotides encoding LT-A or CT-A polypeptides for the
PT transformation of plant cells, useful in immunogenic compositions to
PT elicit immune responses in animals
XX
XX Example 4; Page -: 103pp; English.
XX
XX This is mutant A72R Escherichia coli heat-labile toxin (LT) A subunit
CC (LT-A). The wild-type alanine was replaced with arginine at residue 72
CC of the mature protein, which was caused by a nucleotide change of GC to
CC AG at position 273-274 in the coding sequence. The sequence contains
CC plant-preferred codons and eliminates sequence motifs associated with
CC spurious mRNA processing. A single codon insertion (GTG encoding valine)
CC was made to accommodate the creation of a NcoI restriction site around
CC the initiator methionine codon. Novel polynucleotides encode a mutant
CC LT-A polypeptide or a mutant Vibrio cholerae cholera toxin (CT) A
CC subunit (CT-A) polypeptide, which have reduced enzyme activity as
CC compared to the wild-type LT-A or CT-A polypeptide and where at least one
CC of the codons is altered to a plant preferred codon. The polynucleotide
CC further comprises a nucleic acid sequence encoding LT B subunit (LT-B) or
CC a CT B subunit (CT-B). The polynucleotides are useful for the
CC transformation of plant cells for the production of transgenic plants to
CC produce edible vaccines, especially oral vaccines in transgenic plants
CC for the prophylactic or therapeutic treatment against E. coli or V.
CC cholerae. The mutant polypeptides are also useful as adjuvants.
CC Note: This sequence does not appear in the specification. It was
CC constructed from the wild type LT-A shown in AAY96646 which is given
CC in Figure 1 of the specification.
XX
XX Sequence 259 AA;
SQ
Query Match 48.3%; Score 116; DB 21; Length 259;
Best Local Similarity 100.0%; Pred. No. 5.3e-111;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 73 GOSILSGYSTYIYVIATAPNMFNVDVGVSPHPYEQEVSALGGIPYSQIYGWYRVNF 132
DB 92 gdsilsgystyiyviatapnmfnvndvlgvysphpyeqevsalggipysqiygwrvnf 151
QY 133 GVIDERLHNRREYDRYRNINLAPAEADGYRLAGFPDPDQAWREEPWIHHA PQCGG 188
DB 152 gviderlhnrreaydrdryrnlinaapaedgyrlagfpdpdqawreepwihha pqgcg 207
```

CC	constructed from the wild type LT-A shown in AAY96646 which is given	
XX	in Figure 1 of the specification.	
XX		
50	Sequence	259 AA;
	Query Match	48.3%; Score 116; DB 21; Length 259;
	Best Local Similarity	100.0%; Pred. No. 5.3e-111;
	Matches 116; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	73	QGSILSGYSTVYIVVIATAPNMFNVNDVLGYSPHPYEQEVSALGGIPYSQIYIGWYRVNF 132
Db	92	qgsilsgystyiyviatapnmfndvlgvysphpyeqevsalggipysqiygyrvnf 151
Qy	133	GVIDERLHRNREYRDYRNRUNINIAPAEDGYRLAGPPDHQAWREEPWIHHAQCQG 188
Db	152	gviderlhrnreayrdyrrnliniaaedgyrlagfpdhqawreepwihhpggcg 207
	RESULT 11	
	AAW65074	
ID	AAW65074	standard; protein; 240 AA.
XX	AC	AAW65074;
XX	AC	
DT	11-SEP-1998	(first entry)
XX		
DE	E. coli	LT-A protein fragment.
XX		
KW	Heat labile toxin subunit A; LT-A; mutant; immunogen; detoxification;	
KW	carrier; adjuvant; prevention; treatment; disease; diarrhoea; vaccine;	
KW	infection; enterotoxic.	
XX		
OS	Escherichia coli.	
XX		
FH	Key	Location/Qualifiers
FT	Protein	1..241
FT		/note= "partial sequence"
XX		
PN	WO9818928-A1.	
XX		
PD	07-MAY-1998.	
XX		
PF	30-OCT-1997;	97WO-IB01440.
XX		
PR	31-OCT-1996;	96GB-0022660.
XX		
PA	(CHIR-) CHIRON SPA.	
XX		
PI	Giuliani MM, Pizza M, Rappuoli R;	
XX		
DR	WPI; 1998-272223/24.	
XX		
PT	Mutated Escherichia coli heat labile toxin subunit A - is	
PT	immunogenic and detoxified relative to wild-type, useful e.g. in	
PT	vaccines against E. coli enterotoxigenic strains and as an adjuvant	
XX		
PS	Disclosure; Page -; 67pp; English.	
XX		
CC	This sequence represents a fragment of an Escherichia coli heat labile	
CC	toxin subunit A (LT-A). This protein is used in a method resulting in a	
CC	mutant LT-A protein which has the wild type Ala residue at position 72	
CC	changed to an Arg residue resulting in a toxin which retains its	
CC	immunogenicity but is detoxified. Detoxification is defined in the	
CC	specification as a reduction in toxicity relative to wild-type toxin,	
CC	such that any residual toxicity is sufficiently low to allow use as an	
CC	effective immunogenic composition in humans without significant side	
CC	effects. The protein can be combined with an acceptable carrier in	
CC	immunogenic compositions, optionally comprising an adjuvant and/or a	
CC	second immunogenic antigen. Such compositions can be administered to	
CC	prevent/treat disease in a subject e.g. traveller's diarrhoea in humans.	
CC	The protein or compositions are especially administered as vaccines	
CC	useful to prevent or treat infections by enterotoxigenic strain of	

CC E. coli in mammals (especially humans).

XX Sequence 240 AA;

Query Match 46.2%; Score 111; DB 19; Length 240;

Best Local Similarity 100.0%; Pred. No. 6.9e-106; Mismatches 0; Indels 0; Gaps 0;

Matches 111; Conservative 0;

Qy 1 NGDRLYRADSRPPDEIKRSGGLMPRGHNEYFDRTQNMNINLYDHARGTQTGCFVRYDDGYV 60

|||||

Db 1 ngdrlyradsrppdeikrsgglmpRGHNEYfdRtqnmnInlydhArgTqtGcfvryddgyv 60

|||||

Qy 61 STSLSLRAHLAGOSILSGYSTYIYVIATAPNMFNVNDVLGVYSPHPYEQ 111

|||||

Db 61 stslslrsahlagsilsgystyIyviAtapnmfnvndvlgvysphpyeq 111

RESULT 12

AAW65075

ID AAW65075 standard; protein; 240 AA.

XX AC AAW65075;

XX DT 11-SEP-1998 (first entry)

XX DE E. coli LT-A mutant A72R protein fragment.

XX KW Heat labile toxin subunit A; LT-A; mutant; immunogen; detoxification; carrier; adjuvant; prevention; treatment; disease; diarrhoea; vaccine; infection; enterotoxic.

XX OS Escherichia coli.

XX FH Key Location/Qualifiers

FT Misc-difference 72 /label= A72R

FT /note= "Wild type Ala residue is replaced by Arg"

FT WC9818928-A1.

XX PN 07-MAY-1998.

XX PD 30-OCT-1997; 97WO-IB01440.

XX PF 31-OCT-1996; 96GB-0022660.

XX PR (CHIR-) CHIRON SPA.

XX PA Giuliani MM, Pizza M, Rappuoli R;

XX PI WPI; 1998-272223/24.

XX DR Mutated Escherichia coli heat labile toxin subunit A - is

XX PT immunogenic and detoxified relative to wild-type, useful e.g. in

XX PT vaccines against E. coli enterotoxigenic strains and as an adjuvant

XX PS Claim 3; Page 7; 67pp; English.

XX CC This sequence represents a fragment of a mutant Escherichia coli heat

XX CC labile toxin subunit A (LT-A) where the wild type Ala residue at

XX CC position 72 is replaced by an Arg residue resulting in a toxin which

XX CC retains its immunogenicity but is detoxified. Detoxification is defined

XX CC in the specification as a reduction in toxicity relative to wild-type

XX CC toxin, such that any residual toxicity is sufficiently low to allow use

XX CC as an effective immunogenic composition in humans without significant

XX CC side effects. The protein can be combined with an acceptable carrier in

XX CC immunogenic compositions, optionally comprising an adjuvant and/or a

XX CC second immunogenic antigen. Such compositions can be administered to

XX CC prevent/treat disease in a subject e.g. traveller's diarrhoea in humans.

XX CC The protein or compositions are especially administered as vaccines

XX CC useful to prevent or treat infections by enterotoxigenic strain of

XX CC E. coli in mammals (especially humans).

CC NOTE: This sequence does not appear in the specification but has

CC been constructed from the wild-type sequence represented in AAW65074.

SQ Sequence 240 AA;

Query Match 41.2%; Score 99; DB 19; Length 240;

Best Local Similarity 100.0%; Pred. No. 1.6e-93;

Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 142 NREVRDYVYENLATAEDGCVRLAGFPDHOAWPEEPIHHAPCGGNSRTITGDFCNE 201

|||||

Db 142 nreyrdyrynlnlapeadgyrlagfpdhoawpeepihhApGcgnsrtitgdtcne 201

|||||

Qy 202 ETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIDEL 240

|||||

Db 202 etqnlstiylyreyqskvkrqifsdysqvdiynrirdel 240

RESULT 13

AAAR44016

ID AAR44016 standard; Protein; 236 AA.

XX AC AAR44016;

XX DT 08-DEC-1993 (first entry)

XX DE "Lys-63" E.coli heat labile toxin subunit A.

XX KW enterotoxigenic bacteria; vaccine; immunogenic detoxified LT-A; protomer A; site-directed mutagenesis; reduced toxicity;

XX KW ADP-ribosyltransferase activity.

XX OS Escherichia coli.

XX FH Key Location/Qualifiers

FT Misc-difference 62

FT /note= "corresponds to position 63 in cholera toxin

FT A subunit; wild-type Ser is substituted by

FT Lys to reduce toxicity"

FT WC9313202-A.

XX PD 08-JUL-1993.

XX PF 30-DEC-1992; 92WO-EP03016.

XX PR 31-DEC-1991; 91IT-OMI3513.

XX PA (BIOC-) BIOGINE SCLAVO SPA.

XX PI Domenighini M, Hol W, Pizza M, Rappuoli R;

XX DR WPI; 1993-227320/28.

XX DR N-PSDB; AA051317.

XX PT Immunogenic detoxified mutant cholera toxin and heat labile toxin

XX PT - useful as vaccines against infection by Vibrio cholerae and

XX PT enterotoxin producing Escherichia coli

XX PS Claim 3; Fig 2 and Page 46; 60pp; English.

XX CC The wild-type sequence coding for the A subunit of the heat labile

XX CC toxin (LT-A) of a strain of E.coli known to affect humans (Yamamoto

XX CC et al, J Biol. Chem. 259, 5037-5044 - see AA042768) was subjected to

XX CC site-directed mutagenesis. Certain mutations were found to reduce to

XX CC toxicity (see AAR38730-32 and AAR44016-R44023). The invention relates to

XX CC immunogenic, detoxified LT-A proteins and their use in vaccines to

XX CC protect against enterotoxigenic E.coli. The amino acid sequence of

XX CC this preferred detoxified muten is not printed in the

XX CC specification but has been assembled from the full-length wild-type

XX CC sequence and the description given in the text. (N.B. Amino

XX CC acid numbering is based on the cholera toxin A subunit sequence).

Query Match 35.8%; Score 86; DB 14; Length 236;
Best Local Similarity 100.0%; Pred. No. 3.7e-80;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 103 VYSPHPYEQEVSALGGIPYSOIYGWYRVNFGVIDERLHRNREYRDRYRNINIAPAEDGY 162
Db 99 VYSPHPYEQEVSALGGIPYSOIYGWYRVNFGVIDERLHRNREYRDRYRNINIAPAEDGY 158
Oy 163 RLAGFPDPDQAWREEPWIHHAPOGCG 188
Db 159 RLAGFPDPDQAWREEPWIHHAPOGCG 184

Search completed: June 10, 2002, 17:36:16
Job time: 223 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 10, 2002, 17:33:24 ; Search time 19.04 Seconds
(without alignments)
1211.210 Million cell updates/sec

Title: US-09-297-171-1
Perfect score: 240
Sequence: 1 NGDRLRADSRPPDEIKRSG.....QIFSDYQSEVDIYNRIDEL 240

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Word size : 8

Total number of hits satisfying chosen parameters: 8

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	184	76.7	258	1 QLECA	heat-labile entero
2	27	11.2	125	2 A61345	heat-labile entero
3	26	10.8	258	1 XVVCA	cholera enterotoxi
4	9	3.8	46	2 S39239	cholera enterotoxi
5	8	3.3	782	2 D84514	dynamin-like prote
6	8	3.3	905	1 P3XRA4	inner capsid prote
7	8	3.3	1130	2 T23104	hypothetical prote
8	8	3.3	1133	2 T23103	hypothetical prote

ALIGNMENTS

RESULT 1
QLECA
heat-labile enterotoxin A precursor - Escherichia coli
C:Species: Escherichia coli
C:Date: 30-Apr-1981 #sequence_revision 17-Oct-1997 #text_change 18-Jun-1999
C:Accession: I55231; A01817; A26946
R:Yamamoto, T.; Tamura, T.; Yokota, T.
J. Biol. Chem. 259, 5037-5044, 1984
A:Title: Primary structure of heat-labile enterotoxin produced by Escherichia coli pathd
A:Reference number: I55231; MUID:84185610
A:Accession: I55231
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-258 <RES>
A:Cross-references: GB:K01995; NID:g148027; PIDN:AAA24685.1; PID:g148028
R:Spicer, E.K.; Noble, J.A.

J. Biol. Chem. 257, 5716-5721, 1982
A:Title: Escherichia coli heat-labile enterotoxin. Nucleotide sequence of the A subun
A:Reference number: A01817; MUID:82167425
A:Accession: A01817
A:Molecule type: DNA
A:Residues: 1-21, 'R', 23-36, 'FRS', 40-44, 46-92, 'Y', 94-99, 'LTIYI', 105-107, 111-118, 'IS', 1
A:Cross-references: EMBL:V00275; NID:941339; PIDN:CAA23532.1; PID:941340
A:Note: the authors translated the codon TAR for residue 93 as Ser
R:Yamamoto, T.; Gojobori, T.; Yokota, T.
J. Bacteriol. 169, 1352-1357, 1987
A:Title: Evolutionary origin of pathogenic determinants in enterotoxigenic Escherichl
A:Reference number: A26946; MUID:87137303
A:Accession: A26946
A:Molecule type: DNA
A:Residues: 1-21, 'R', 23-206, 'N', 208-230, 'E', 232-255, 'D', 257-258 <YAM>
A:Cross-references: EMBL:M15363
C:Comment: The heat-labile enterotoxin molecule contains one A chain and five or six
class.
C:Genetics:
A:Gene: eta
C:Superfamily: heat-labile enterotoxin chain A
C:Keywords: enterotoxin
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-258/Product: heat-labile enterotoxin chain A #status predicted <MAT>

Query Match 76.7%; Score 184; DB 1; Length 258;
Best Local Similarity 100.0%; Pred. No. 4.2e-190;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTGTGTVRYDDGVVSTSL 64
|||||
DB 23 LYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTGTGTVRYDDGVVSTSL 82
|||||
QY 65 SLRSAHLAGQSILSGSYTYIYVIATAPNMENVDVGVSPHPYEQEVSALGGIPYSQI 124
|||||
DB 83 SLRSAHLAGQSILSGSYTYIYVIATAPNMENVDVGVSPHPYEQEVSALGGIPYSQI 142
|||||
QY 125 YGWYRVNFGVIDERLHRNREYRDYRNLTAPAEEDGYRLAGFPDPHQWREEPWIHAP 184
|||||
DB 143 YGWYRVNFGVIDERLHRNREYRDYRNLTAPAEEDGYRLAGFPDPHQWREEPWIHAP 202
|||||
QY 185 QGCG 188
|||||
DB 203 QGCG 206

RESULT 2
A61345
heat-labile enterotoxin A chain precursor - Escherichia coli (fragments)
C:Species: Escherichia coli
C:Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 17-Mar-1999
C:Accession: A61345
R:Spicer, E.K.; Kavanaugh, W.M.; Dallas, W.S.; Falkow, S.; Konigsberg, W.H.; Schafer,
Proc. Natl. Acad. Sci. U.S.A. 78, 50-54, 1981
A:Title: Sequence homologies between a subunits of Escherichia coli and Vibrio cholera
A:Reference number: A61345; MUID:81223767
A:Accession: A61345
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-125 <SPI>
A:Cross-references: GB:K00433
A:Note: authors translated the codon GAG for residue 27 as Asp, CAA for residue 53 as
C:Superfamily: heat-labile enterotoxin chain A

Query Match 11.2%; Score 27; DB 2; Length 125;
Best Local Similarity 100.0%; Pred. No. 3.5e-21;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 NEYFDRGTQMNINLYDHARGTGTGTVR 54
|||||
DB 45 NEYFDRGTQMNINLYDHARGTGTGTVR 71

RESULT 3

XVCA
cholera enterotoxin chain A precursor Vcl1457 [validated] - Vibrio cholerae
C:Species: Vibrio cholerae
C:Date: 06-Jul-1982 #sequence_revision 26-Jan-1996 #text_change 01-Sep-2000
C:Accession: A05129; S14623; S14625; A91268; A91746; A92298; S17665; B43864; A82
R:Mekalanos, J.J.; Swartz, D.J.; Pearson, G.D.N.; Harford, N.; Groyne, F.; de Wilde, M.
Nature 306, 551-557, 1983
A:Reference number: A93320; MUID:84068199
A:Accession: A05129
A:Molecule type: DNA
A:Residues: 1-258 <MEK>
R:Dams, E.; de Wolf, M.; Dierick, W.
submitted to the EMBL Data Library, March 1991
A:Description: Correction of the cholera toxin nucleotide sequence of the Vibrio cholera
A:Reference number: S14623
A:Accession: S14623
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-258 <DA2>
A:CROSS-references: EMBL:X58785; NID:g48420; PIDN:CAA41592.1; PID:g48421
A:Experimental source: strain 2125
A:Accession: S14625
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-258 <DA2>
A:CROSS-references: EMBL:X58785; NID:g48888; PIDN:CAA41590.1; PID:g48889
A:Experimental source: strain 569B
R:Lai, C.Y.; Cancedda, F.; Chang, D.
FEBS Lett. 100, 85-89, 1979
A:Title: Primary structure of cholera toxin subunit A-1. Isolation, partial sequences an
A:Reference number: A91268; MUID:79169830
A:Accession: A91268
A:Molecule type: protein
A:Residues: 37-38, 'L', 40-44, 'SE', 47-49, 'B', 51-55, 'B', 57, 'B', 59-60, 'B', 62-66, 'Z', 68-72, 'I
R:Duffy, L.K.; Peterson, J.W.; Kurosky, A.
FEBS Lett. 126, 187-190, 1981
A:Title: Isolation and characterization of a precursor form of the 'A' subunit of cholera
A:Reference number: A91286; MUID:81212799
A:Accession: A91286
A:Molecule type: protein
A:Residues: 19, 'N', 21-27 <DUF>
R:Klapper, D.G.; Finkelstein, R.A.; Capra, J.D.
Immunochimistry 13, 605-611, 1976
A:Title: Subunit structure and N-terminal amino acid sequence of the three chains of cho
A:Reference number: A91746; MUID:76259136
A:Accession: A91746
A:Molecule type: protein
A:Residues: 19-36, 'R', 38, 213-232 <KUA>
R:Duffy, L.K.; Peterson, J.W.; Kurosky, A.
J. Biol. Chem. 256, 12252-12256, 1981
A:Title: Covalent structure of the gamma chain of the A subunit of cholera toxin.
A:Reference number: A92298; MUID:82053094
A:Accession: A92298
A:Molecule type: protein
A:Residues: 213-246, 'ID', 249-255, 'N', 257-258 <DU2>
R:Dams, E.; de Wolf, M.; Dierick, W.
Biochim. Biophys. Acta 1090, 139-141, 1991
A:Title: Nucleotide sequence analysis of the CT operon of the Vibrio cholerae classical
A:Reference number: S17665; MUID:91355224
A:Accession: S17665
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-258 <DAM>
A:CROSS-references: EMBL:X58785; NID:g48888; PIDN:CAA41590.1; PID:g48889
R:Baudry, B.; Fasano, A.; Kettley, J.; Kaper, J.B.
Infect. Immun. 60, 428-434, 1992
A:Title: Cloning of a gene (zot) encoding a new toxin produced by Vibrio cholerae.
A:Reference number: A43864; MUID:92112300
A:Accession: B43864
A>Status: preliminary

A:Molecule type: DNA
A:Residues: 1-6 <BAU>
A:CROSS-references: GB:M83563; NID:gl55314; PIDN:AAA27583.1; PID:gl55316
A:Note: sequence extracted from NCBI backbone (NCBIN:77488, NCBIP:77496)
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Winn, M.L.; Dodson, R.
chardson, D.; Emolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoli, I.; Seller
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833
A:Accession: A82197
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-258 <HEI>
A:CROSS-references: GB:AE004224; GB:AE003852; NID:g9655952; PIDN:AAF94614.1; GSPDB:G
A:Experimental source: serogroup O1; strain Ni9661; biotype El Tor
C:Genetics:
A:Gene: Vcl1457
A:Map position: 1
C:Complex: the cholera enterotoxin molecule contains three kinds of chains; an alpha
ciate noncovalently with the subunit B, an aggregate of five beta chains
C:Function:
A:Description: the active component of the toxin that is primarily responsible for E
.2.5) activity also activates intracellular adenyl cyclase
C:Superfamily: heat-labile enterotoxin chain A
C:Keywords: enterotoxin
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-212/Product: cholera enterotoxin alpha chain #status experimental <CTA>
F:213-258/Product: cholera enterotoxin gamma chain #status experimental <CTG>
F:217/Disulfide bonds: interchain (to alpha chain) #status predicted

Query Match 10.8%; Score 26; DB 1; Length 258;
Best Local Similarity 100.0%; Pred. No. 8.1e-20;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 EYFDRGTQNNINLYDHARGTQTGFVR 54
|||||
Db 47 EYFDRGTQNNINLYDHARGTQTGFVR 72
|||||

RESULT 4
S39239
cholera enterotoxin chain A2 - Vibrio cholerae (serotype 0139)
N:Alternate names: CTA2 cholera toxin chain A2
C:Species: Vibrio cholerae
A:Variety: serotype 0139
C:Date: 08-May-1995 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C:Accession: S39239; S39240
R:Lebens, M.; Holmgren, J.
submitted to the EMBL Data Library, November 1993
A:Description: Structure and arrangement of the Cholera toxin genes in vibrio Cholera
A:Reference number: S39238
A:Accession: S39239
A:Molecule type: DNA
A:Residues: 1-46 <LEB>
A:CROSS-references: EMBL:X76390; NID:g433856; PIDN:CAA53974.1; PID:g433858; EMBL:X763
A:Experimental source: strain 4260B; serotype 0139
C:Superfamily: heat-labile enterotoxin chain A

Query Match 3.8%; Score 9; DB 2; Length 46;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 213 EYQSKVKRQ 221
|||||
Db 19 EYQSKVKRQ 27
|||||

RESULT 5
D84514
dynamain-like protein [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: D84514
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: D84514
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-782 <SPO>
A:Cross-references: GB:AE002093; MID:g4587686; PIDN:AAD25856.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g14120
A:Map position: 2

Query Match 3.3%; Score 8; DB 2; Length 782;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 204 QNLSTIYL 211
|
Db 628 QNLSTIYL 635

RESULT 6

P3XRA4

Inner capsid protein VP3 - African horse sickness virus (serotype 4)

C:Species: African horse sickness virus
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 07-May-1999
C:Accession: B44053
R:Iwata, H.; Yamagawa, M.; Roy, P.
Virology 191, 251-261, 1992
A:Title: Evolutionary relationships among the gnat-transmitted orbiviruses that cause African horse sickness.

A:Reference number: A44053; MUID:93033117

A:Accession: B44053

A:Molecule type: genomic RNA

A:Residues: 1-905 <IWA>

A:Cross-references: GB:M94681

C:Superfamily: bluetongue virus core protein VP3

C:Keywords: capsid protein

Query Match 3.3%; Score 8; DB 1; Length 905;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DSRPPDEI 16
|
Db 791 DSRPPDEI 798

RESULT 7

T23104

hypothetical protein H19N07.2b - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T23104

R:Dobson, R.

submitted to the EMBL Data Library, March 1997

A:Reference number: Z19678

A:Accession: T23104

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1130 <WIL>

A:Cross-references: EMBL:Z92835; PIDN:CAB07397.1; GSPDB:GN00023; CESP:H19N07.2b

A:Experimental source: clone H19N07

C:Genetics:

A:Gene: CESP:H19N07.2b

A:Map position: 5
A:Introns: 71/2; 183/2; 339/1; 659/3; 699/1; 963/2; 998/3; 1080/3; 1105/1

Query Match 3.3%; Score 8; DB 2; Length 1130;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 137 ERLHRNRE 144
|
Db 529 ERLHRNRE 536

RESULT 8

T23103

hypothetical protein H19N07.2a - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T23103

R:Dobson, R.

submitted to the EMBL Data Library, March 1997

A:Reference number: Z19678

A:Accession: T23103

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1133 <WIL>

A:Cross-references: EMBL:Z92835; PIDN:CAB07396.1; GSPDB:GN00023; CESP:H19N07.2a

A:Experimental source: clone H19N07

C:Genetics:

A:Gene: CESP:H19N07.2a

A:Map position: 5

A:Introns: 71/2; 183/2; 339/1; 659/3; 699/1; 963/2; 1001/3; 1083/3; 1108/1

Query Match 3.3%; Score 8; DB 2; Length 1133;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 137 ERLHRNRE 144
|
Db 529 ERLHRNRE 536

Search completed: June 10, 2002, 17:37:01
Job time: 217 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 10, 2002, 17:36:39 ; Search time 11.04 Seconds
(without alignments)
841.729 Million cell updates/sec

Title: US-09-297-171-1
Perfect score: 240
Sequence: 1 NGDRLYRADSRPPDEIKRSG.....QIFSDYQSEVDIYNRDEL 240

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0
Searched: 105224 seqs, 38719550 residues
Word size : 8
Total number of hits satisfying chosen parameters: 6

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	240	100.0	258	1 ELAP_ECOLI	P06717 escherichia
2	208	86.7	258	1 ELAH_ECOLI	P43530 escherichia
3	26	10.8	258	1 CHTA_VIBCH	P01555 vibrio chol
4	11	4.6	263	1 E2BA_ECOLI	P43528 escherichia
5	8	3.3	905	1 VP3_AHSV4	P32509 african hor
6	8	3.3	905	1 VP3_AHSV6	O71025 african hor

ALIGNMENTS

```
RESULT 1
ELAP_ECOLI
ID ELAP_ECOLI STANDARD; PRT; 258 AA.
AC P06717; P01554;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Heat-labile enterotoxin A chain precursor (LT-A, porcine) (LTP-A).
GN ELTA OR LTPA.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RC STRAIN=ISOLATE PCG86, AND ISOLATE P307;
RX MEDLINE=87137303; Pubmed=3546273;
RA Yamamoto T., Gojobori T., Yokota T.;
RT "Evolutionary origin of pathogenic determinants in enterotoxigenic
RT Escherichia coli and Vibrio cholerae O1.";
RL J. Bacteriol. 169:1352-1357(1987).
RN [2]
```


Submitted (MAY-1991) to the EMBL/GenBank/DBJ databases.
 [5]
 SEQUENCE FROM N.A.
 STRAIN=KNIH002;
 Shin H.J., Park Y.C., Kim Y.C.;
 "Cloning and nucleotide sequence analysis of the virulence gene
 cassette from *Vibrio cholerae* KNH002 isolated in Korea.;"
 Misalinmuhag Hoiji 35:205-210(1999).
 [6]
 SEQUENCE FROM N.A.
 STRAIN=EL TOR N16961 / SEROTYPE O1;
 MEDLINE=20406833; Pubmed=10952301;
 Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
 Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
 McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
 Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 Fraser C.M.;
 "DNA sequence of both chromosomes of the cholera pathogen *Vibrio*
cholerae.;"
 Nature 406:477-483(2000).
 [7]
 SEQUENCE OF 1-212 FROM N.A.
 STRAIN=CLASSICAL 569B / ATCC 25870 / SEROTYPE O1;
 MEDLINE=85006737; Pubmed=6090390;
 Lockman H.A., Gaten J.E., Kaper J.B.;
 "Vibrio cholerae enterotoxin genes: nucleotide sequence analysis of
 DNA encoding ADP-ribosyltransferase.;"
 J. Bacteriol. 159:1086-1089(1984).
 [8]

RA MEDLINE=84061784; PubMed=6033707;
RA Lockman H., Kaper J.B.;
RT "Nucleotide sequence analysis of the A2 and B subunits of *Vibrio*
RT cholerae enterotoxin.";
RL J. Biol. Chem. 258:13722-13726(1983).
RN [9]
RN SEQUENCE OF 19-27.
RX MEDLINE=81212799; PubMed=7238869;
RA Duffy L.K., Peterson J.W., Kurosky A.;
RT "Isolation and characterization of a precursor form of the 'A'
RT subunit of cholera toxin.";
RL FEBS Lett. 126:187-190(1981).
RN [10]
RN SEQUENCE OF 19-38 AND 213-232.
RX MEDLINE=76259136; PubMed=955672;
RA Klapper D.G., Finkelstein R.A., Capra J.D.;
RT "Subunit structure and N-terminal amino acid sequence of the three
RT chains of cholera enterotoxin.";
RL Immunochimistry 13:605-611(1976).
RN [11]
RN SEQUENCE OF 27-72 AND 111-139.
RX MEDLINE=79169830; PubMed=437113;
RA Lai C.-Y., Cancedda F., Chang D.;
RT "Primary structure of cholera toxin subunit A1: Isolation, partial
RT sequences and alignment of the BCn fragments.";
RL FEBS Lett. 100:85-89(1979).
RN [12]
RN SEQUENCE OF 213-258.
RX MEDLINE=82053094; PubMed=7028752;
RA Duffy L.K., Peterson J.W., Kurosky A.;
RT "Covalent structure of the gamma chain of the A subunit of cholera
RT toxin.";
RL J. Biol. Chem. 256:12252-12256(1981).
RN [13]
RN X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
RX MEDLINE=95387395; PubMed=7658473;
RA Zhang R.G., Scott D.L., Westbrook M.L., Nance S., Spangler B.D.,
RA Shipley G.G., Westbrook E.M.;
RT "The three-dimensional crystal structure of cholera toxin.";
RL J. Mol. Biol. 251:563-573(1995).
RN CC -1- FUNCTION: THE ALPHA/GAMMA CHAIN (A SUBUNIT) IS AN ADP-RIBOSYLATING

hemorrhagic disease as evidenced by their capsid protein sequences.";
 Virology 191:251-261(1992).

OC SEQUENCE FROM N.A.
 RX STRAIN-VACCINE;
 RA MEDLINE=94270993; PubMed=8002793;
 RA Sakamoto K., Punyahotra R., Mizukoshi N., Ueda S., Imagawa H.,
 RA Sugura T., Kanada M., Fukusho A.,
 RT "Rapid detection of African horsesickness virus by the reverse
 RT transcriptase polymerase chain reaction (RT-PCR) using the ampImer
 RT for segment 3 (VP3 gene).";
 RL Arch. Virol. 136:87-97(1994).
 CC -1- FUNCTION: THE VP3 PROTEIN IS ONE OF THE FIVE PROTEINS (WITH VP1,
 CC VP4, VP6 AND VP7) WHICH FORM THE INNER CAPSID OF THE VIRUS.
 CC -1- SIMILARITY: BELONGS TO THE REOVIRUSES VP3 FAMILY.
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 CC -----
 CC EMBL; M94681; AAA42538.1; ALT_SEQ.
 DR EMBL; D26572; BAA05621.1; -.
 DR PIR; B44053; P3XRA4.
 DR HSP; P56582; 2BT.
 DR InterPro; IPR002614; Orbi_VP3.
 DR Pfam; PF01700; Orbi_VP3; 1.
 DR ProDom; PD004438; Orbi_VP3; 1.
 KW Core protein.
 FT CONFLICT 17 18 YA -> LS (IN REF. 1).
 FT CONFLICT 25 25 S -> D (IN REF. 1).
 FT CONFLICT 121 121 I -> V (IN REF. 1).
 FT CONFLICT 195 195 I -> V (IN REF. 1).
 FT CONFLICT 231 231 Q -> P (IN REF. 1).
 FT CONFLICT 253 253 F -> S (IN REF. 1).
 FT CONFLICT 403 408 RALSDV -> AALTI (IN REF. 1).
 FT CONFLICT 446 456 DPOTGRYNGW -> THKRVGLORV (IN REF. 2).
 FT CONFLICT 560 560 F -> L (IN REF. 1).
 FT CONFLICT 662 662 F -> P (IN REF. 1).
 FT CONFLICT 708 708 Y -> T (IN REF. 1).
 FT CONFLICT 732 732 Y -> H (IN REF. 1).
 FT CONFLICT 802 850 MPVYTEERDGRVMAFKYATATAYFLYNNVAYSTPTPT
 FT LITVNTPT -> IANQANMGQFAAIRRTLDNGWIQFGG
 FT MLRNKIKFFDSRPDEILT (IN REF. 1).
 FT V -> L (IN REF. 1).
 FT R -> A (IN REF. 1).
 FT I -> V (IN REF. 1).
 SQ SEQUENCE 905 AA; 103328 MW; 92D8C3C8FAB957A0 CRC64;

Query Match 3.3%; Score 8; DB 1; Length 905;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DSRPDEI 16
 Db 791 DSRPDEI 798
 |||||

RESULT 6
 VP3_AHSV6 STANDARD; PRT; 905 AA.
 AC O71025;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE VP3 core protein.
 GN S3 OR L3.
 OS African horse sickness virus 6 (AHSV-6) (African horse sickness virus
 (serotype 6)).

OC Viruses: dsRNA viruses; Reoviridae; Orbivirus.
 OX NCBI_TaxID=86060;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98278331; PubMed=9617769;
 RA Williams C.F., Inoue T., Lucas A.-M., Zanotto P., Roy P.;
 RT "The complete sequence of four major structural proteins of African
 RT horse sickness virus serotype 6: evolutionary relationships within
 RT and between the orbiviruses.";
 RL Virus Res. 53:53-73(1998).
 CC -1- FUNCTION: THE VP3 PROTEIN IS ONE OF THE FIVE PROTEINS (WITH VP1,
 CC VP4, VP6 AND VP7) WHICH FORM THE INNER CAPSID OF THE VIRUS.
 CC -1- SIMILARITY: BELONGS TO THE REOVIRUSES VP3 FAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF021236; AAC40995.1; -.
 DR HSP; P56582; 2BT.
 DR InterPro; IPR002614; Orbi_VP3.
 DR Pfam; PF01700; Orbi_VP3; 1.
 DR ProDom; PD004438; Orbi_VP3; 1.
 KW Core protein.
 SQ SEQUENCE 905 AA; 103305 MW; 8748565C70D9B90C CRC64;

Query Match 3.3%; Score 8; DB 1; Length 905;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DSRPDEI 16
 Db 791 DSRPDEI 798
 |||||

Search completed: June 10, 2002, 17:40:08
 Job time: 209 sec

" "

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 10, 2002, 17:36:19 ; Search time 26.46 Seconds
(without alignments)
1569.115 Million cell updates/sec

Title: US-09-297-171-1
Perfect score: 240
Sequence: 1 NGRRLRADSRPPDEIKRSG.....QIFSDYQSEVDIYNIRDEL 240

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

Word size : 8

Total number of hits satisfying chosen parameters: 11

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

- Database :
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_rvirus:*
 - 16: sp_bacteriaph:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	191	79.6	258	2	O66280 escherichia
2	24	10.0	68	2	Q47182 escherichia
3	9	3.8	46	2	Q57372 vibrio chol
4	8	3.3	309	17	Q9HJH5 thermoplasm
5	8	3.3	330	17	Q97AR5 thermoplasm
6	8	3.3	616	12	P87708 fowlpox vir
7	8	3.3	782	10	Q9S147 arabidopsis
8	8	3.3	903	12	Q64928 african hor
9	8	3.3	1130	5	O45624 caenorhabdi
10	8	3.3	1133	5	O45623 caenorhabdi
11	8	3.3	1766	12	Q9J599 fowlpox vir

ALIGNMENTS

```
RESULT 1
O66280
ID O66280 PRELIMINARY; PRT; 258 AA.
AC O66280;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE HEAT-LABILE ENTEROTOXIN A SUBUNIT.
GN LTH A SUBUNIT.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1032 (ENTEROTOXIGENIC);
RA Komase K.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=1032 (ENTEROTOXIGENIC);
RX MEDLINE=95091056; PubMed=7998417;
RA Tamura S., Asanuma H., Tomita T., Komase K., Kawahara K., Danbara H.,
RA Hattori N., Watanabe K., Suzuki Y., Nagamine T., Aizawa C., Oya A.,
RA Kurata T.;
RT "Escherichia coli heat-labile enterotoxin B subunits supplemented with
a trace amount of the holotoxin as an adjuvant for nasal influenza
vaccine.";
RL Vaccine 12:1083-1089(1994).
DR EMBL; AB011677; BAA25725.1; -.
DR HSP; P06717; ILTG
DR InterPro; IPR001144; Enterotoxin_A.
DR InterPro; IPR000886; ER_target.
DR Pfam; PF01375; Enterotoxin_A; 1.
DR PRINTS; PR00771; ENTEROTOXINA.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN.1.
SQ SEQUENCE 258 AA; 29931 MW; 2BB15D27740EB788 CRC64;

Query Match 79.6%; Score 191; DB 2; Length 258;
Best Local Similarity 100.0%; Pred. No. 2.8e-186;
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMINLYDHARGTQTGFVRVDDGVYSTSL 64
Db 23 LYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMINLYDHARGTQTGFVRVDDGVYSTSL 82
Qy 65 SLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLCVYSPHPYQEVSVSALGGIPYSQI 124
Db 83 SLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLCVYSPHPYQEVSVSALGGIPYSQI 142
Qy 125 YGWYRVNFGVIDERLHNRNREYRDYRNLTAPAEADGYRLAGFPDPDQWREPEWIHAP 184
Db 143 YGWYRVNFGVIDERLHNRNREYRDYRNLTAPAEADGYRLAGFPDPDQWREPEWIHAP 202
Qy 185 QGCGNSSRTIT 195
Db 203 QGCGNSSRTIT 213

RESULT 2
Q47182 PRELIMINARY; PRT; 68 AA.
ID Q47182
AC Q47182;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ENTEROTOXIN A (FRAGMENT).
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
```

```
RP SEQUENCE OF 64-68 FROM N.A.
RC STRAIN-H10407;
RX MEDLINE=83007048; PubMed=6749816;
RA Yamamoto T., Tamura T., Yoji M., Kaji A., Yokota T., Takano T.;
RT "Sequence analysis of the heat-labile enterotoxin subunit B gene
RL originating in human enterotoxigenic Escherichia coli.";
RN J. Bacteriol. 152:506-509(1982).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN-H10407;
RX MEDLINE=83114628; PubMed=6759877;
RA Yamamoto T., Tamura T., Yokota T., Takano T.;
RT "Overlapping genes in the heat-labile enterotoxin operon originating
RL from Escherichia coli human strain.";
RN Mol. Gen. Genet. 188:356-359(1982).
[3]
RP SEQUENCE OF 64-68 FROM N.A.
RC STRAIN-H10407;
RX MEDLINE=83265593; PubMed=6348025;
RA Yamamoto T., Yokota T.;
RT "Sequence of heat-labile enterotoxin of Escherichia coli pathogenic
RL for humans.";
RN J. Bacteriol. 155:728-733(1983).
DR EMBL: J01646; AAB02981.1;
DR HSP: P06717; I1T3
DR InterPro: IPR001144; Enterotoxin_A.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF01375; Enterotoxin_A; 1.
DR PRINTS: PR00771; ENTEROTOXINA.
DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 68 AA; 8077 MW; 673CDE4D2E884854 CRC64;

Query Match 10.0%; Score 24; DB 2; Length 68;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 214 YQSKVKRQIFSDYQSEVDIYNRIR 237
Db 42 YQSKVKRQIFSDYQSEVDIYNRIR 65

RESULT 3
Q57372 PRELIMINARY; PRT; 46 AA.
AC Q57372;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CHOLERA TOXIN A2.
GN CTXA2.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=4260B;
RX MEDLINE=94237453; PubMed=8181723;
RA Lebers M., Holmgren J.;
RT "Structure and arrangement of the cholera toxin genes in Vibrio
RL FEMS Microbiol. Lett. 117:197-202(1994).
DR EMBL: X76391; CAA53975.1;
DR EMBL: X76390; CAA53974.1;
DR HSP: P01555; I1T3.
DR InterPro: IPR001144; Enterotoxin_A.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF01375; Enterotoxin_A; 1.
DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
SQ SEQUENCE 46 AA; 5447 MW; 1B6085A02E8889D6 CRC64;
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Query Match 3.8%; Score 9; DB 2; Length 46;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 213 EYOSKVKRQ 221
Db 19 EYOSKVKRQ 27

RESULT 4
Q9HJH5 PRELIMINARY; PRT; 309 AA.
AC Q9HJH5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE HYPOTHETICAL MEMBRANE PROTEIN.
GN TA0993.
OS Thermoplasma acidophilum.
OC Archaea; Euryarchaeota; Thermoplasmatales; Thermoplasmaceae;
OC Thermoplasma.
OX NCBI_TaxID=2303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 1728;
RX MEDLINE=20479972; PubMed=11029001;
RA Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
RA Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
RT "The genome sequence of the thermoacidophilic scavenger Thermoplasma
RT acidophilum.";
RL Nature 407:508-513(2000).
DR EMBL: AL445066; CAC12122.1;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 309 AA; 33633 MW; C39F9882B276B380 CRC64;

Query Match 3.3%; Score 8; DB 17; Length 309;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 YIYIVAT 90
Db 94 YIYIVAT 101

RESULT 5
Q97AR5 PRELIMINARY; PRT; 330 AA.
AC Q97AR5;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DE TVG0750122 PROTEIN.
GN TVG0750122.
OS Thermoplasma volcanium.
OC Archaea; Euryarchaeota; Thermoplasmatales; Thermoplasmaceae;
OC Thermoplasma.
OX NCBI_TaxID=50339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GSSI / DSM 4299 / JCM 9571;
RX MEDLINE=20570466; PubMed=11121031;
RA Kawashima T., Amano N., Koike H., Yamazaki M., Kanehori K., Kawamoto T.,
RA Kawashima-Ohya Y., Watanabe K., Yamakino H., Makino S.-I., Higuchi S.,
RA Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;
RT "Archaeal adaptation to higher temperatures revealed by genomic
RL sequence of Thermoplasma volcanium.";
RN Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
DR EMBL: AP000993; BAB59886.1;
KW Complete proteome.
SQ SEQUENCE 330 AA; 35912 MW; 22DD4CCB803B61BB CRC64;
```

Query Match 3.3%; Score 8; DB 17; Length 330;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 YYIXVIAT 90
 |||||

Db 113 YYIVVIAT 120

RESULT 6

ID P87708 PRELIMINARY; PRT; 616 AA.
 AC P87708;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE ORF1 AND ORF2 GENES, ORF3 AND ORF4 GENES (FRAGMENT).
 OS Fowlpox virus (FPV).
 OS Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Avipoxvirus.
 OX NCBI_TaxID=10261;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-TCP-BLEN (CEVA);
 RA Stefancsik R., Rauch T.;
 RT "Fowlpox virus TCP-BLEN (CEVA).";
 RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U17141; ABA40513.1;
 DR InterPro: IPR002029; Peptidase_S8.
 DR PROSITE: PS00136; SUBTILASE_ASP; UNKNOWN_1.
 FT NON_TER 616
 SQ SEQUENCE 616 AA; 68545 MW; 3177A67B8520B24A CRC64;

Query Match 3.3%; Score 8; DB 12; Length 616;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 SILSGYST 82
 |||||

Db 272 SILSGYST 279

RESULT 7

ID Q9S147 PRELIMINARY; PRT; 782 AA.
 AC Q9S147;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE DYNAMIN-LIKE PROTEIN.
 GN AT2G14120.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RX MEDLINE=20083487; PubMed=10617197;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
 RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
 RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
 RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
 RA Copenhaver G.P., Preuss D., Niemann W.C., White O., Eisen J.A.,
 RA Salzberg S.L., Fraser C.M., Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 thaliana.";
 RL Nature 402:761-768(1999).
 RN [2]
 RP SEQUENCE FROM N.A.

RC STRAIN=CV. COLUMBIA;
 RA Lin X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC007197; AAD25856.1;
 DR InterPro: IPR001401; Dynamlin.
 DR InterPro: IPR000375; Dynamlin_central.
 DR InterPro: IPR003130; GED.
 DR Pfam: PF00350; dynamlin.1.
 DR Pfam: PF01031; dynamlin_2; 1.
 DR Pfam: PF02122; GED; 1.
 DR PRINTS; PR00195; DYNAMIN.
 DR SMART; SM00553; DYNc; 1.
 DR SMART; SM00302; GED; 1.
 SQ SEQUENCE 782 AA; 86862 MW; 6789A588734EC051 CRC64;

Query Match 3.3%; Score 8; DB 10; Length 782;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 QNLSTIYL 211
 |||||

Db 628 QNLSTIYL 635

RESULT 8

ID Q64928 PRELIMINARY; PRT; 903 AA.
 AC Q64928;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE INNER SHELL PROTEIN.
 GN VP3.
 OS African horse sickness virus.
 OC Viruses; dsRNA viruses; Reoviridae; Orbivirus.
 OX NCBI_TaxID=10896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Alonso J.L., Martinez J.L., Casal J.I.;
 RT "Nucleotide sequence of the African horsesickness virus L3 gene.";
 RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
 DR EMBL: M94312; AAA42542.1;
 DR HSP: P56582; 2BT.
 DR InterPro: IPR002614; Orbi_VP3.
 DR Pfam: PF01700; Orbi_VP3; 1.
 DR PRODOM: PD004438; Orbi_VP3; 1.
 SQ SEQUENCE 903 AA; 102980 MW; B261DAEF08EA42AA CRC64;

Query Match 3.3%; Score 8; DB 12; Length 903;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DSRPPDEI 16
 |||||

Db 789 DSRPPDEI 796

RESULT 9

ID Q45624 PRELIMINARY; PRT; 1130 AA.
 AC Q45624;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE H19N07.2B PROTEIN.
 GN H19N07.2B.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]

RP SEQUENCE FROM N.A.
RA Dobson R.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-99069613; PubMed-9351916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z92835; CAB07397.1; -;
DR MEROPS; C19.UPW; -;
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR002083; MATH.
DR InterPro; IPR001394; UCH-2.
DR Pfam; PF00917; MATH; 1.
DR Pfam; PF00442; UCH-1; 1.
DR Pfam; PF00443; UCH-2; 1.
DR SMART; SM00061; MATH; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS00972; UCH_2_1; 1.
DR PROSITE; PS00973; UCH_2_2; 1.
DR PROSITE; PS50235; UCH_2_3; 1.
SQ SEQUENCE 1130 AA; 131082 MW; FCF498B7925A570 CRC64;

Query Match 3.3%; Score 8; DB 5; Length 1130;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 ERLHNRRE 144
Db 529 ERLHNRRE 536
|||||

RESULT 10
ID 045623 PRELIMINARY; PRT; 1133 AA.
AC 045623;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE H19N07.2A PROTEIN.
GN H19N07.2A.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Dobson R.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-99069613; PubMed-9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z92835; CAB07396.1; -;
DR MEROPS; C19.UPW; -;
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR002083; MATH.
DR InterPro; IPR001394; UCH-2.
DR Pfam; PF00917; MATH; 1.
DR Pfam; PF00442; UCH-1; 1.
DR Pfam; PF00443; UCH-2; 1.
DR SMART; SM00061; MATH; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS00972; UCH_2_1; 1.
DR PROSITE; PS00973; UCH_2_2; 1.
DR PROSITE; PS50235; UCH_2_3; 1.
SQ SEQUENCE 1133 AA; 131355 MW; 6742C643285C6025 CRC64;

Query Match 3.3%; Score 8; DB 5; Length 1133;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 ERLHNRRE 144
Db 529 ERLHNRRE 536
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RESULT 11
ID 09J599 PRELIMINARY; PRT; 1766 AA.
AC 09J599;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ORF FPV123 VARIOLA B22R GENE FAMILY PROTEIN.
GN FPV123.
OS Fowlpox virus (FPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Avipoxvirus.
OX NCBI_TaxID=10261;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20193820; PubMed-10729156;
RA Afonso C.L., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
RT "The genome of fowlpox virus.";
RL J. Virol. 74:3815-3831(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Afonso C.L., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF198100; AAF44467.1; -;
DR InterPro; IPR000209; Peptidase_S8.
DR PROSITE; PS00136; SUBTILASE_ASP; UNKNOWN_1.
SQ SEQUENCE 1766 AA; 201146 MW; B3D87FF4A52679D9 CRC64;

Query Match 3.3%; Score 8; DB 12; Length 1766;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 SILSGYST 82
Db 728 SILSGYST 735
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Search completed: June 10, 2002, 17:39:51
Job time: 212 sec

OLIGO - INTERFERENCE

us-09-297-171-1-oligo.ra1

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 10, 2002, 17:33:09 ; Search time 13.05 Seconds
(without alignments)
449.206 Million cell updates/sec

Title: US-09-297-171-1
Perfect score: 240
Sequence: 1 NGDRLYRADSRPPDEIKRSG.....QIFSDYQSEVDIYNRDEL 240

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 231628 seqs, 24425594 residues

Word size : 8

Total number of hits satisfying chosen parameters: 49

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA: *
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4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	188	78.3	240	4	US-08-823-120-3
2	86	35.8	236	4	US-08-823-120-6
3	86	35.8	254	3	US-08-486-099-114
4	86	35.8	254	3	US-08-360-107A-124
5	86	35.8	254	3	US-08-484-223B-114
6	86	35.8	254	3	US-08-919-597-114
7	86	35.8	254	3	US-08-475-668A-114
8	86	35.8	254	3	US-08-485-511A-114
9	86	35.8	254	3	US-08-471-913A-114
10	86	35.8	254	4	US-08-485-264A-114
11	86	35.8	254	4	US-08-474-349A-114
12	26	10.8	179	2	US-08-435-605A-57
13	26	10.8	192	2	US-08-435-605A-6
14	26	10.8	194	2	US-08-435-605A-6
15	26	10.8	194	2	US-08-435-605A-14
16	26	10.8	194	2	US-08-435-605A-16
17	26	10.8	194	2	US-08-435-605A-54
18	26	10.8	194	2	US-08-435-605A-55
19	26	10.8	238	4	US-08-823-120-2
20	26	10.8	240	2	US-08-435-605A-13
21	26	10.8	240	2	US-08-435-605A-15
22	26	10.8	240	2	US-08-435-605A-50
23	26	10.8	240	2	US-08-435-605A-51
24	26	10.8	240	2	US-08-435-605A-52
25	26	10.8	240	2	US-08-435-605A-53
26	26	10.8	240	2	US-08-435-605A-56
27	26	10.8	240	4	US-08-823-120-4

28	26	10.8	240	4	US-08-823-120-8	Sequence 8, Appli
29	26	10.8	258	1	US-08-449-045C-2	Sequence 2, Appli
30	26	10.8	258	2	US-08-435-605A-2	Sequence 2, Appli
31	26	10.8	258	6	5223610-2	Patent No. 5223610
32	22	9.2	240	2	US-08-435-605A-49	Sequence 49, Appli
33	20	8.3	20	1	US-08-171-299B-11	Sequence 11, Appli
34	15	6.2	15	3	US-08-296-848A-2	Sequence 2, Appli
35	12	5.0	12	2	US-08-292-968-7	Sequence 7, Appli
36	12	5.0	12	2	US-08-467-974-7	Sequence 7, Appli
37	12	5.0	12	2	US-08-467-536-7	Sequence 7, Appli
38	12	5.0	12	3	US-08-467-976-7	Sequence 7, Appli
39	12	5.0	12	4	US-09-082-514-7	Sequence 7, Appli
40	12	5.0	46	2	US-08-435-605A-10	Sequence 10, Appli
41	9	3.8	9	2	US-08-292-968-8	Sequence 8, Appli
42	9	3.8	9	2	US-08-467-974-8	Sequence 8, Appli
43	9	3.8	9	2	US-08-467-536-8	Sequence 8, Appli
44	9	3.8	9	3	US-08-467-976-8	Sequence 8, Appli
45	9	3.8	9	4	US-09-082-514-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-08-823-120-3
; Sequence 3, Application US/08823120
; Patent No. 6149919
; GENERAL INFORMATION:
; APPLICANT: Domenighini, Mario
; APPLICANT: Rappuoli, Rino
; APPLICANT: Pizza, Mariagrazia
; TITLE OF INVENTION: Immunogenic Detoxified Mutants of
; TITLE OF INVENTION: Cholera Toxin and of the Toxin It, Their Preparation and
; TITLE OF INVENTION: Their Use for the Preparation of Vaccines
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: California
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/823,120
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/256,003
; FILING DATE: 11-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: McClung, Barbara G.
; REGISTRATION NUMBER: 33,113
; REFERENCE/DOCKET NUMBER: 0315.001
; TELEPHONE: (510) 601-2708
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-823-120-3

Query Match 78.3%; Score 188; DB 4; Length 240;
Best Local Similarity 100.0%; Pred. No. 1.8e-181;

Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NGRDLYRADSRPDEIKRSGGLMPRGHNEYFDRCTQMNLYDHARGTGTGFVRYDDGYV 60
Db 1 NGRDLYRADSRPDEIKRSGGLMPRGHNEYFDRCTQMNLYDHARGTGTGFVRYDDGYV 60

Qy 61 STSLSLSAHLAGOSILSGYSTYYIYVIATAPNMFNVNDVLGYSPHPYQEVSAALGGIP 120
Db 61 STSLSLSAHLAGOSILSGYSTYYIYVIATAPNMFNVNDVLGYSPHPYQEVSAALGGIP 120

Qy 121 YSQIYGWYRVNFGVIDERLHNRNREYRDYRYNRLNIAPAEDGYRLAGFPDQHWAREEPWI 180
Db 121 YSQIYGWYRVNFGVIDERLHNRNREYRDYRYNRLNIAPAEDGYRLAGFPDQHWAREEPWI 180

Qy 181 HHAPQGGC 188
Db 181 HHAPQGGC 188

RESULT 2
US-08-823-120-6
; Sequence 6, Application US/08823120
; Patent No. 6149919
; GENERAL INFORMATION:
; APPLICANT: Domenighini, Mario
; APPLICANT: Rappuoli, Rino
; APPLICANT: Piazza, Mariagrazia
; TITLE OF INVENTION: Immunogenic Detoxified Mutants of
; TITLE OF INVENTION: Cholera Toxin and of the Toxin Lt, Their Preparation and
; TITLE OF INVENTION: Their Use for the Preparation of Vaccines
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: California
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/823,120
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/256,003
; FILING DATE: 11-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: McClung, Barbara G.
; REGISTRATION NUMBER: 33,113
; REFERENCE/DOCKET NUMBER: 0315.001
; TELEPHONE: (510) 601-2703
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-823-120-6

Query Match 35.8%; Score 86; DB 4; Length 236;
Best Local Similarity 100.0%; Pred. No. 7.8e-79;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 103 VYSPHPYQEVSAALGGIPYSQIYGWYRVNFGVIDERLHNRNREYRDYRYNRLNIAPAEDGY 162
Db 99 VYSPHPYQEVSAALGGIPYSQIYGWYRVNFGVIDERLHNRNREYRDYRYNRLNIAPAEDGY 158

Qy 163 RLAGFPDQHWAREEPWIHHAPQGGC 188
Db 159 RLAGFPDQHWAREEPWIHHAPQGGC 184

RESULT 3
US-08-486-099-114
; Sequence 114, Application US/08486099
; Patent No. 6013263
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
; TITLE OF INVENTION: B VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,099
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-486-099-114

Query Match 35.8%; Score 86; DB 3; Length 254;
Best Local Similarity 100.0%; Pred. No. 8.3e-79;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 103 VYSPHPYQEVSAALGGIPYSQIYGWYRVNFGVIDERLHNRNREYRDYRYNRLNIAPAEDGY 162
Db 117 VYSPHPYQEVSAALGGIPYSQIYGWYRVNFGVIDERLHNRNREYRDYRYNRLNIAPAEDGY 176

Qy 163 RLAGFPDQHWAREEPWIHHAPQGGC 188
Db 177 RLAGFPDQHWAREEPWIHHAPQGGC 202

RESULT 4
US-08-360-107A-124
; Sequence 124, Application US/08360107A
; Patent No. 6017536

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/919,597
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470,896
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-919-597-114

Query Match 35.8%; Score 86; DB 3; Length 254;
Best Local Similarity 100.0%; Pred. No. 8.3e-79;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 VYSPHPYEQEVSALGGIPYSQIYGWYRVNFGVIDERLHRNREYRDYRNLTAPADGY 162
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DB 117 VYSPHPYEQEVSALGGIPYSQIYGWYRVNFGVIDERLHRNREYRDYRNLTAPADGY 176
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QY 163 RLAGFPDPHQAWREPWIHAFQCG 188
|||||
DB 177 RLAGFPDPHQAWREPWIHAFQCG 202
|||||

RESULT 7
US-08-475-668A-114
Sequence 114, Application US/08475668A
Patent No. 6060065
GENERAL INFORMATION:
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,668A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-475-668A-114

Query Match 35.8%; Score 86; DB 3; Length 254;
Best Local Similarity 100.0%; Pred. No. 8.3e-79;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 VYSPHPYEQEVSALGGIPYSQIYGWYRVNFGVIDERLHRNREYRDYRNLTAPADGY 162
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DB 117 VYSPHPYEQEVSALGGIPYSQIYGWYRVNFGVIDERLHRNREYRDYRNLTAPADGY 176
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QY 163 RLAGFPDPHQAWREPWIHAFQCG 188
|||||
DB 177 RLAGFPDPHQAWREPWIHAFQCG 202
|||||

RESULT 8
US-08-485-551A-114
Sequence 114, Application US/08485551A
Patent No. 6068973
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,551A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-023
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
TYPE: amino acid
STRANDEDNESS:

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;       TOPOLOGY: unknown
;       MOLECULE TYPE: protein
US-08-485-551A-114

Query Match          35.8%; Score 86; DB 3; Length 254;
Best Local Similarity 100.0%; Pred. No. 8.3e-79;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 VYSPHPYEQEVSALGGIPYSQIYGWYRVNFGVIDERLHRNREYDRYRNLIAPAEDGY 162
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Db 117 VYSPHPYEQEVSALGGIPYSQIYGWYRVNFGVIDERLHRNREYDRYRNLIAPAEDGY 176
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QY 163 RLAGFPDPHQAWREEPWIHPAQCGG 188
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Db 177 RLAGFPDPHQAWREEPWIHPAQCGG 202
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RESULT 9
US-08-471-913A-114
; Sequence 114, Application US/08471913A
; Patent No. 6093794
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 214
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,913A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-471-913A-114

Query Match          35.8%; Score 86; DB 3; Length 254;
Best Local Similarity 100.0%; Pred. No. 8.3e-79;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 VYSPHPYEQEVSALGGIPYSQIYGWYRVNFGVIDERLHRNREYDRYRNLIAPAEDGY 162
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Db 117 VYSPHPYEQEVSALGGIPYSQIYGWYRVNFGVIDERLHRNREYDRYRNLIAPAEDGY 176
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QY 163 RLAGFPDPHQAWREEPWIHPAQCGG 188
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Db 177 RLAGFPDPHQAWREEPWIHPAQCGG 202
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RESULT 11
US-08-474-349A-114
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Db 117 VYSPHPYEQEVSALGGIPYSQIYGWYRVNFGVIDERLHRNREYDRYRNLIAPAEDGY 176
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QY 163 RLAGFPDPHQAWREEPWIHPAQCGG 188
|||||
Db 177 RLAGFPDPHQAWREEPWIHPAQCGG 202
|||||

RESULT 10
US-08-485-264A-114
; Sequence 114, Application US/08485264A
; Patent No. 6228983
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
; TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,264A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-485-264A-114

Query Match          35.8%; Score 86; DB 4; Length 254;
Best Local Similarity 100.0%; Pred. No. 8.3e-79;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 VYSPHPYEQEVSALGGIPYSQIYGWYRVNFGVIDERLHRNREYDRYRNLIAPAEDGY 162
|||||
Db 117 VYSPHPYEQEVSALGGIPYSQIYGWYRVNFGVIDERLHRNREYDRYRNLIAPAEDGY 176
|||||
QY 163 RLAGFPDPHQAWREEPWIHPAQCGG 188
|||||
Db 177 RLAGFPDPHQAWREEPWIHPAQCGG 202
|||||

RESULT 11
US-08-474-349A-114
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[illegible]

Sequence 114, App
Sequence 114, App
Sequence 114, App
Sequence 114, App

sequence 114, App
sequence 6, Appli
sequence 2, Appli

Sequence 4, Appli
Sequence 8, AppliSequence 4, Appli
Sequence 8, Appli

Sequence 48, Appl

Sequence 52, Appl

Sequence 48, Appl

Sequence 52, Appl

Sequence 4, Appli

Sequence 2, Appl1

Sequence 7, Appli
Sequence 2, AppliSequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli

3
4
5
6
7

507

100

LT-A TOXIN

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h 240;
s 0; Gaps 0;
GFVRYDDGYV 60
|||||
GFVRYDDGYV 60
```

h 240;

s 0; Gaps 0;

GFVRYDDGYV 60
|||||
GFVRYDDGYV 60

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Qy 61 STSLSLSAHLAQSILSGYSTYIIYVIATAPNMFNVDLVGYSPHPYEQEVSALGGIP 120
Db 61 STSLSLSAHLAQSILSGYSTYIIYVIATAPNMFNVDLVGYSPHPYEQEVSALGGIP 120

Qy 121 YSQIYGWYRVNFGVIDERLHRNREYRDYRNLNIAPAEDGYRLAGFPDPHQAWREEPWI 180
Db 121 YSQIYGWYRVNFGVIDERLHRNREYRDYRNLNIAPAEDGYRLAGFPDPHQAWREEPWI 180

Qy 181 HHAPOGCGNSRTTGTCTCNEETQNLSTIYLREYQSKVKQIFSDYQSEVDIYNRIDEL 240
Db 181 HHAPOGCGNSRTTGTCTCNEETQNLSTIYLREYQSKVKQIFSDYQSEVDIYNRIDEL 240

RESULT 2
US-08-256-003-3
; Sequence 3, Application US/08256003
; GENERAL INFORMATION:
; APPLICANT: Domenighini, Mario
; APPLICANT: Rappuoli, Rino
; APPLICANT: Piazza, Mariagrazia
; TITLE OF INVENTION: Immunogenic Detoxified Mutants of
; TITLE OF INVENTION: Cholera Toxin and of the Toxin Lt, Their Preparation and
; TITLE OF INVENTION: Their Use for the Preparation of Vaccines
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: California
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,003
; FILING DATE: 11-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McClung, Barbara G.
; REGISTRATION NUMBER: 33,113
; REFERENCE/DOCKET NUMBER: 0315.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2708
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-256-003-3

Query Match 78.3%; Score 188; DB 6; Length 240;
Best Local Similarity 100.0%; Pred. No. 1.1e-185;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NGRDLRADSRPPDEIKRSGGLMPRGHNEYFDRGTOMNINLYDHARGTQTGFVRYDDGYV 60
Db 1 NGRDLRADSRPPDEIKRSGGLMPRGHNEYFDRGTOMNINLYDHARGTQTGFVRYDDGYV 60

Qy 61 STSLSLSAHLAQSILSGYSTYIIYVIATAPNMFNVDLVGYSPHPYEQEVSALGGIP 120
Db 61 STSLSLSAHLAQSILSGYSTYIIYVIATAPNMFNVDLVGYSPHPYEQEVSALGGIP 120

Qy 121 YSQIYGWYRVNFGVIDERLHRNREYRDYRNLNIAPAEDGYRLAGFPDPHQAWREEPWI 180
Db 121 YSQIYGWYRVNFGVIDERLHRNREYRDYRNLNIAPAEDGYRLAGFPDPHQAWREEPWI 180
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Qy 181 HHAPQCGC 188
Db 181 HHAPQCGC 188

RESULT 3
PCT-US99-30747-4
; Sequence 4, Application PC/TUS9930747
; GENERAL INFORMATION:
; APPLICANT: Boyce Thompson Institute for Plant Research at Cor
; TITLE OF INVENTION: Orally Immunogenic Bacterial Enterotoxins Expressed In
; TITLE OF INVENTION: Transgenic Plants
; FILE REFERENCE: 4868/85427
; CURRENT APPLICATION NUMBER: PCT/US99/30747
; CURRENT FILING DATE: 1999-12-22
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:E. coli
; OTHER INFORMATION: heat-labile toxin gene mutagenized to optimize
; OTHER INFORMATION: expression in plants.
PCT-US99-30747-4

Query Match 76.7%; Score 184; DB 1; Length 259;
Best Local Similarity 100.0%; Pred. No. 1.6e-181;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LYRADSRPPDEIKRSGGLMPRGHNEYFDRGTOMNINLYDHARGTQTGFVRYDDGYVSTSL 64
Db 24 LYRADSRPPDEIKRSGGLMPRGHNEYFDRGTOMNINLYDHARGTQTGFVRYDDGYVSTSL 83

Qy 65 SLRSAHLAQSILSGYSTYIIYVIATAPNMFNVDLVGYSPHPYEQEVSALGGIPYSQI 124
Db 84 SLRSAHLAQSILSGYSTYIIYVIATAPNMFNVDLVGYSPHPYEQEVSALGGIPYSQI 143

Qy 125 YGWYRVNFGVIDERLHRNREYRDYRNLNIAPAEDGYRLAGFPDPHQAWREEPWIHAP 184
Db 144 YGWYRVNFGVIDERLHRNREYRDYRNLNIAPAEDGYRLAGFPDPHQAWREEPWIHAP 203

Qy 185 QCGC 188
Db 204 QCGC 207

RESULT 4
US-09-470-124-4
; Sequence 4, Application US/09470124
; GENERAL INFORMATION:
; APPLICANT: Mason
; APPLICANT: Arntzen
; TITLE OF INVENTION: Orally Immunogenic Bacterial Enterotoxins Expressed In
; TITLE OF INVENTION: Transgenic Plants
; FILE REFERENCE: 4868/84454
; CURRENT APPLICATION NUMBER: US/09/470,124
; CURRENT FILING DATE: 1999-12-24
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:E. coli
; OTHER INFORMATION: heat-labile toxin gene mutagenized to optimize
; OTHER INFORMATION: expression in plants.
US-09-470-124-4
```



```
; NAME: HARBIN, ALISA A.
; REGISTRATION NUMBER: 33,895
; REFERENCE/DOCKET NUMBER: 1393.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 655-8730
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-044-696-2

Query Match 35.8%; Score 86; DB 14; Length 236;
Best Local Similarity 100.0%; Pred. No. 5e-80;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 VYSPHPYEQEVSALGGIPYSQIYGWYRVNFGVIDERLHNRNREYDRYRNLNIAPAEDGY 162
Db 99 VYSPHPYEQEVSALGGIPYSQIYGWYRVNFGVIDERLHNRNREYDRYRNLNIAPAEDGY 158
QY 163 RLAGFPDPHQAWREPWIIHAPOGCG 188
Db 159 RLAGFPDPHQAWREPWIIHAPOGCG 184

RESULT 8
US-08-360-107-124
; Sequence 124, Application US/08360107
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,107
; FILING DATE: 20-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 124:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; STRANDEDNESS:
; TYPE: amino acid
; TOPOLOGY: unknown
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; MOLECULE TYPE: protein
US-08-360-107-124

Query Match 35.8%; Score 86; DB 7; Length 254;
Best Local Similarity 100.0%; Pred. No. 5.4e-80;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 VYSPHPYEQEVSALGGIPYSQIYGWYRVNFGVIDERLHNRNREYDRYRNLNIAPAEDGY 162
Db 117 VYSPHPYEQEVSALGGIPYSQIYGWYRVNFGVIDERLHNRNREYDRYRNLNIAPAEDGY 176
QY 163 RLAGFPDPHQAWREPWIIHAPOGCG 188
Db 177 RLAGFPDPHQAWREPWIIHAPOGCG 202

RESULT 9
US-08-470-896-114
; Sequence 114, Application US/08470896
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,896
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-470-896-114

Query Match 35.8%; Score 86; DB 8; Length 254;
Best Local Similarity 100.0%; Pred. No. 5.4e-80;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 VYSPHPYEQEVSALGGIPYSQIYGWYRVNFGVIDERLHNRNREYDRYRNLNIAPAEDGY 162
Db 117 VYSPHPYEQEVSALGGIPYSQIYGWYRVNFGVIDERLHNRNREYDRYRNLNIAPAEDGY 176
```

QY 163 RLAGFPDHOAWREEPWIHAPQCG 188
|||||
Db 177 RLAGFPDHOAWREEPWIHAPQCG 202

RESULT 10

US-08-471-913-114
; Sequence 114, Application US/08471913
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-471-913-114

Query Match 35.8%; Score 86; DB 8; Length 254;

Best Local Similarity 100.0%; Pred. No. 5.4e-80;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 VYSPHPYEQVVSALGIPYSQIYGWYRVNFGVIDERLHRNREYDRYRNLTAPAEDGY 162
|||||

Db 117 VYSPHPYEQVVSALGIPYSQIYGWYRVNFGVIDERLHRNREYDRYRNLTAPAEDGY 176
|||||

RESULT 11

US-08-475-668-114
; Sequence 114, Application US/08475668
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.

; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA
; TITLE OF INVENTION: VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,668
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-475-668-114

Query Match 35.8%; Score 86; DB 8; Length 254;

Best Local Similarity 100.0%; Pred. No. 5.4e-80;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 VYSPHPYEQVVSALGIPYSQIYGWYRVNFGVIDERLHRNREYDRYRNLTAPAEDGY 162
|||||

Db 117 VYSPHPYEQVVSALGIPYSQIYGWYRVNFGVIDERLHRNREYDRYRNLTAPAEDGY 176
|||||

QY 163 RLAGFPDHOAWREEPWIHAPQCG 188
|||||

Db 177 RLAGFPDHOAWREEPWIHAPQCG 202
|||||

RESULT 12

US-08-484-223-114
; Sequence 114, Application US/08484223
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-484-223A-114

Query Match 35.8%; Score 86; DB 8; Length 254;
Best Local Similarity 100.0%; Pred. No. 5.4e-80;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 163 VYSPHPYEQEVSALGGIPYSIQIYGWYRVNFGVIDERLHRNREYRDRYRNLTAPAEDGY 162
|||||
Db 117 VYSPHPYEQEVSALGGIPYSIQIYGWYRVNFGVIDERLHRNREYRDRYRNLTAPAEDGY 176
|||||
QY 163 RLAGFPDQHWREPWIIHAPGCG 188
|||||
Db 177 RLAGFPDQHWREPWIIHAPGCG 202

RESULT 13
US-08-484-223A-114
; Sequence 114, Application US/08484223A
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-484-223A-114

Query Match 35.8%; Score 86; DB 8; Length 254;
Best Local Similarity 100.0%; Pred. No. 5.4e-80;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 VYSPHPYEQEVSALGGIPYSIQIYGWYRVNFGVIDERLHRNREYRDRYRNLTAPAEDGY 162
|||||
Db 117 VYSPHPYEQEVSALGGIPYSIQIYGWYRVNFGVIDERLHRNREYRDRYRNLTAPAEDGY 176
|||||
QY 163 RLAGFPDQHWREPWIIHAPGCG 188
|||||
Db 177 RLAGFPDQHWREPWIIHAPGCG 202

RESULT 14
US-08-485-546-114
; Sequence 114, Application US/08485546
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,546
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-485-546-114

Query Match 35.8%; Score 86; DB 8; Length 254;
Best Local Similarity 100.0%; Pred. No. 5.4e-80;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 103 VYSPHPYEQEVSALGGIPYSQIYGWRYNFGVIDERLHRNREYDRYRNLIAPAEDGY 162
Db 117 VYSPHPYEQEVSALGGIPYSQIYGWRYNFGVIDERLHRNREYDRYRNLIAPAEDGY 176
Qy 163 RLAGFPDPHQAWREEPWIHHAPOCGG 188
Db 177 RLAGFPDPHQAWREEPWIHHAPOCGG 202

RESULT 15
US-08-485-546A-114
Sequence 114, Application US/08485546A
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,546A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-028
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-485-546A-114

Query Match 35.8%; Score 86; DB 8; Length 254;
Best Local Similarity 100.0%; Pred. No. 5.4e-80;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 103 VYSPHPYEQEVSALGGIPYSQIYGWRYNFGVIDERLHRNREYDRYRNLIAPAEDGY 162
Db 117 VYSPHPYEQEVSALGGIPYSQIYGWRYNFGVIDERLHRNREYDRYRNLIAPAEDGY 176
Qy 163 RLAGFPDPHQAWREEPWIHHAPOCGG 188
Db 177 RLAGFPDPHQAWREEPWIHHAPOCGG 202

Search completed: June 10, 2002, 17:38:55
Job time: 216 sec


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RESULT      1
US-59-528-682-1
; Sequence 1, Application US/09528682
; GENERAL INFORMATION:
; APPLICANT: Pizza, Mariagrazia
; APPLICANT: Giuliani, Rinzia M
; APPLICANT: Rappuoli, Rino
; TITLE OF INVENTION: IMMUNOGENIC DETOXIFIED MUTANT E. COLI LT-A-TOXIN
; FILE REFERENCE: 2302-0342.10
; CURRENT APPLICATION NUMBER: US/09528, 682
; CURRENT FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: PCT/IB97/01440
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: 09/297,171
; PRIOR FILING DATE: 1999-04-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0

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